

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:19:50 ; Search time 37 Seconds

(without alignments)
28.605 Million cell updates/sec

Title: US-10-088-681-1

Perfect Score: 60

Sequence: 1 TGSFSELMWS 11

Scoring table: BLOSSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

1328

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	50.0	10	2 C39191	hypothetical protein
2	24	40.0	7	2 PH1602	Ig H chain V-D-J r
3	23	38.3	10	2 T13838	cytochrome-c
4	20	33.3	6	2 B34835	oxida
5	20	33.3	11	2 S05002	dna protein - Pse
6	19	31.7	6	2 PT0519	corazonin - Americ
7	19	31.7	6	2 A3129	T-cell receptor beta
8	19	31.7	8	2 A41117	neuropeptide GNFR
9	19	31.7	9	2 S626850	acetylcholinester
10	18	30.0	9	2 S07241	Ig heavy chain v r
11	18	30.0	10	2 C41946	Litorin - Rohde s
12	18	30.0	10	2 S31789	T-cell receptor ga
13	18	30.0	11	1 LFTWWE	neuropeptide Pec-H
14	18	30.0	11	2 S33300	probable trpG lea
15	17.5	29.2	8	2 JS0315	probable substance
16	17	28.3	7	2 PT0586	leukokinin V - Mad
17	17	28.3	8	2 A44960	T-cell receptor be
18	17	28.3	8	2 S08995	neuropeptide Leed-C
19	17	28.3	8	2 A49823	hypertrehalosemic
20	17	28.3	8	2 A33976	adipokinetic hormo
21	17	28.3	8	2 B43976	hypertrehalosemic
22	17	28.3	8	2 A05169	neuropeptide M-1 -
23	17	28.3	10	2 A10561	hypertrehalosemic
24	16	26.7	4	2 PT0661	t-cell receptor be
25	16	26.7	7	4 I55382	hypothetical pepti
26	16	26.7	8	2 A12523	peptidyl-dipeptida
27	16	26.7	8	2 S11545	adipokinetic hormo
28	16	26.7	8	2 A61348	red pigment-concen
29	16	26.7	8	2 A28004	adipokinetic hormo

RESULT 1
C39191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis

C;Species: Bacteroides fragilis

C;Date: 08-Nov-1991 #text_change 08-Nov-1991 #text_change 30-Sep-1993

C;Accession: C39191

R;Speer, B.S.; Bedzyk, L.; Salyers, A.A.

J. Bacteriol. 173, 176-183, 1991

A;Title: Evidence for a novel tetracycline resistance gene found on two Bacteroides tr:

A;Reference number: A39191; MUID:91100280; PMID:1846135

A;Accession: C39191

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <SPEL>

A;Cross-references: GB:M37699

Query Match 50.0%;
Best Local Similarity 62.5%;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PFSELWTS 11
Db 2 YFSRPWTIS 9

RESULT 2
PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1602

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-322, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice

A;Reference number: PH1580; MUID:93301609; PMID:93301609

A;Accession: PH1602

A;Molecule type: DNA

A;Residues: 1-7 <IEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 40.0%;
Best Local Similarity 80.0%;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SELWT 10
Db 3 SSLWT 7

RESULT 3
T13838

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Bipes biperus* mitochondrion (fragment)
 C;Species: mitochondrion *Bipes biperus*
 C;Accession: R13838
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A;Reference number: Z17799; PMID:97153846; PMID:900057
 A;Accession: R13838
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-10 <MAC>
 A;Cross-references: UNIPROT:P92576; EMBL:U71335; NID:91753232; PID:91753235; PIDN:AB482
 A;Genome: mitochondrial
 A;Note: COI
 C;Keywords: mitochondrion; oxidoreductase

Query Match	Score	Length	Pred.	No.	Gaps	Indels	Conservative	Mismatches	Matches	Indels	Gaps
Qy 1 TGSFPS 6	38.3%	23	DB 2;	Score 23;	Length 10;				5	0;	0;
Db 4 TRSFFS 9	83.3%	0;	DB 2;	Pred. No. 3.6e+02;	Length 10;				5	0;	0;

RESULT 4
 B34835
 draA Protein - *Pseudomonas aeruginosa* (fragment)
 C;Species: *Pseudomonas aeruginosa*
 C;Accession: B34835
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 R;Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Escherichia coli
 A;Reference number: A34835; MUID:90160310; PMID:2106132
 A;Accession: B34835
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <YEE>
 A;Cross-references: GB:M30125; NID:9151419; PIDN:AAA225916.1; PID:9151421
 C;Keywords: DNA binding

Query Match	Score	Length	Pred.	No.	Gaps	Indels	Conservative	Mismatches	Matches	Indels	Gaps
Qy 7 ELW 9	33.3%	20	DB 2;	Score 20;	Length 6;				5	0;	0;
Db 4 ELW 6	100.0%	0;	DB 2;	Pred. No. 2.8e+05;	Length 6;				5	0;	0;

RESULT 5
 S05002
 coronozin - American cockroach
 C;Species: *Periplaneta americana* (American cockroach)
 C;Accession: S05002
 C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
 R;Veenstra, J.A.
 FEBS Lett. 250, 231-234, 1989
 A;Title: Isolation and structure of coronozin, a cardioactive peptide from the american cockroach
 A;Reference number: S05002; MUID:99325572; PMID:2753332
 A;Accession: S05002
 A;Molecule type: protein
 A;Residues: 1-11 <REB>
 A;Cross-references: UNIPROT:P11496
 A;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;1/Modified site: amidated carboxyl end (Asn) #status experimental
 Query Match
 Best Local Similarity 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;

RESULT 6
 PR0519
 T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PR0519
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PR0509; MUID:91277601; PMID:1711558
 A;Accession: PR0519
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-6 <SPEE>
 A;Experimental source: adult thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match	Score	Length	Pred.	No.	Gaps	Indels	Conservative	Mismatches	Matches	Indels	Gaps
Qy 6 SELW 9	31.7%	19	DB 2;	Score 19;	Length 6;				5	0;	0;
Db 2 SSLW 5	75.0%	0;	DB 2;	Pred. No. 2.8e+05;	Length 6;				5	0;	0;

RESULT 7
 A43129
 neuropeptide GNFRamide - tapeworm (*Nonniezia expansa*)
 C;Species: *Nonniezia expansa*
 C;Accession: A43129
 C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
 R;Mauli, A.; Shaw, C.; Halton, D.; Thim, L.
 Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
 A;Title: GNFRamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm
 A;Reference number: A43129; MUID:93312289; PMID:8323331
 A;Accession: A43129
 A;Molecule type: protein
 A;Residues: 1-6 <MAUS>
 A;Cross-references: UNIPROT:P41966
 C;Keywords: amidated carboxyl end; neuropeptide
 F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match	Score	Length	Pred.	No.	Gaps	Indels	Conservative	Mismatches	Matches	Indels	Gaps
Qy 2 GSFF 5	31.7%	19	DB 2;	Score 19;	Length 6;				5	0;	0;
Db 1 GNFF 4	75.0%	0;	DB 2;	Pred. No. 2.8e+05;	Length 6;				5	0;	0;

RESULT 8
 A41117
 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
 C;Species: *Naja naja oxiana* (Asian cobra, *Oxus cobra*)
 C;Accession: A41117
 C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
 R;Kreinkamp, H.J.; Weise, C.; Raba, R.; Aviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo marmorata
 A;Reference number: A41117; MUID:91296772; PMID:2068091
 A;Accession: A41117
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <KRE>

A; Cross-references: UNIPROT:Q7LZ27
 C; Keywords: carboxylic ester hydrolase

Query Match 31.7%; Score 19; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SELW 9
 :||:
 Db 2 AEMW 5 .

RESULT 9

S36850 19 heavy chain V region - mouse
 C; Species: Mus musculus (house mouse)
 C; Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
 R; Jacob, J.; Kelsoe, G.
 submitted to the EMBL Data Library, July 1992
 A; Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
 A; Reference number: S25024
 A; Accession: S36850
 A; Status: preliminary
 A; Molecule type: nucleic acid
 A; Residues: 1-9 <JAC>
 A; Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799_1.; PID:e51594; PID:91333871
 Query Match 31.7%; Score 19; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; Length 9;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GSFF 5
 :||:
 Db 6 GSYF 9

RESULT 10

S07241 Litoria - Rohde's leaf frog
 C; Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C; Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
 R; Barra, D.; Falconieri Ersperer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Ersperer,
 PEBs Lett. 182, 53-56, 1985
 A; Title: Rohdeia litoria: a new Peptide from the skin of Phyllomedusa rohdei.
 A; Reference number: S07241; MUID:85127560; PMID:3838283
 A; Accession: S07241
 A; Molecule type: protein
 A; Residues: 1-9 <BAR>
 A; Cross-references: UNIPROT:PO8946
 C; Superfamily: gastrin-releasing peptide
 C; Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
 F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F; 9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 30.0%; Score 18; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05; Length 9;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 EIWTS 11
 :||:
 Db 1 QLWAT 5

RESULT 11

C41946 T-cell receptor gamma chain (1t.60) - mouse (fragment)
 C; Species: Mus musculus (house mouse)
 C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 R; Whetsell, M.; Mosley, R. L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 S33300

Mol. Cell. Biol. 11, 5902-5909, 1991
 A; Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
 A; Reference number: A41946; MUID:92049316; PMID:1658619
 A; Accession: C41946
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-10 <WHE>
 C; Keywords: T-cell receptor

Query Match 30.0%; Score 18; DB 2; Length 10;
 Best Local Similarity 28.6%; Pred. No. 2.9e+03;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FSBLWTS 11
 :||:
 Db 1 YCAVNS 7

RESULT 12

S53789 neuropeptide Pec-HTH - Platypleura capensis
 C; Species: Platypleura capensis
 C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C; Accession: S53789
 R; Gaede, G.; Janssens, M. P.E.
 A; Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehaloseamide-like activity
 A; Reference number: S53789; MUID:95225385; PMID:7710694
 A; Accession: S53789
 A; Molecule type: protein
 A; Residues: 1-10 <GAE>
 A; Cross-references: UNIPROT:Q7M465
 C; Keywords: blocked amino end; blocked carboxyl end

Query Match 30.0%; Score 18; DB 2; Length 10;
 Best Local Similarity 30.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FSBLW 9
 :||:
 Db 4 FSPSW 8

RESULT 13

LFTWWE probable trpEG leader peptide - Thermus aquaticus
 C; Species: Thermus aquaticus
 C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
 C; Accession: S03315
 R; Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
 Biochim. Biophys. Acta 950, 303-312, 1988
 A; Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and
 A; Reference number: S03315; MUID:89000781; PMID:2844259
 A; Accession: S03315
 A; Molecule type: DNA
 A; Residues: 1-11 <SAT>
 A; Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565_1; PID:g48262
 A; Note: the source is designated as *Thermus thermophilus* HB8
 C; Genetics:
 A; Gene: tPL
 C; Superfamily: probable trpEG leader peptide

Query Match 30.0%; Score 18; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SELW 9
 :||:
 Db 5 SALW 8

RESULT 14

probable substance P - smaller spotted catshark

C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33300

A;Residue: R;Waugh, D.;Wang, Y.;Hazon, N.;Balment, R.J.;Conlon, J.M.

Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from

A;Reference number: S33300; MTRD:93292508; PMID:7655693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAW>

A;Cross-references: UNIPROT:P41333

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gas

A;Note: substance P is derived by post-translational processing of proprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match Score 18;

Best Local Similarity 75.0%; Score 2;

Length 11;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSFF 5

Db 5 QFFF 8

RESULT 15

JS0315

Leucokinin V - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS0315

R;Holman, G.M.;Cook, B.J.;Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic

A;Reference number: JS0315

A;Accession: JS0315

A;Molecule type: protein

A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P19987

C;Comment: Leucokinins, a family of cephalomyotrop peptide, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotrop peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 29.2%;

Best Local Similarity 62.5%; Score 17.5;

Length 8;

Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 2 GSFFSEIW 9

Db 1 GSGFSS-W 7

Search completed: April 27, 2005, 15:30:31

Job time : 38 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:18:52 ; Search time 173 Seconds
(without alignments)

32.560 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSSFSELWTS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : UniProt_03;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	24	40.0	11	2	077895		077895 oreochromis
2	24	40.0	11	2	077896		077896 oreochromis
3	23	38.3	10	2	P92576	bipes bipes	P92576 bipes bipes
4	23	38.3	11	2	P83537	lactobacillus	P83537 lactobacillus
5	21	35.0	9	2	Q95953	homo sapien	Q95953 homo sapien
6	20	33.3	10	2	Q6LA62	homo sapien	Q6LA62 homo sapien
7	20	33.3	11	1	CA42_LITCI		CA42_LITCI
8	20	33.3	11	1	CORZ_PERAM		CORZ_PERAM
9	20	33.3	11	2	077894	periplaneta americana	077894 periplaneta americana
10	20	33.3	11	2	077898	oreochromis	077898 oreochromis
11	19	31.7	6	1	O65CG7	sinaloa tom	O65CG7 sinaloa tom
12	19	31.7	8	2	FARP_MONEY		FARP_MONEY
13	19	31.7	8	2	Q99MNO	mus musculus	Q99MNO mus musculus
14	19	31.7	8	2	Q71Z27	naja okiana	Q71Z27 naja okiana
15	19	31.7	10	2	Q9TR47	bos taurus	Q9TR47 bos taurus
16	19	31.7	10	2	Q8SHC6	furcifer beauforti	Q8SHC6 furcifer beauforti
17	19	31.7	11	2	O9UC46	homo sapien	O9UC46 homo sapien
18	18	30.0	9	1	L1TR_PHYRO	phyllomedusa	P08446 phyllomedusa
19	18	30.0	9	2	Q9h3Y3	homo sapien	Q9h3Y3 homo sapien
20	18	30.0	9	2	Q8H9Z1	cyanophage	Q8h9z1 cyanophage
21	18	30.0	9	2	O9O350	gb virus c/human	O9o350 gb virus c/human
22	18	30.0	10	1	AKHX_LOCM1	locusta migratoria	P81626 locusta migratoria
23	18	30.0	10	1	QTM465	platypleura	Q7m465 platypleura
24	18	30.0	10	2	Q8SHB1	rhampholeon	Q8shb1 rhampholeon
25	18	30.0	10	2	Q8SHB4	furcifer verreauxii	Q8shb4 furcifer verreauxii
26	18	30.0	10	2	Q8SHB7	furcifer oustaleti	Q8shb7 furcifer oustaleti
27	18	30.0	10	2	Q8SHC0	furcifer laevigatus	Q8shc0 furcifer laevigatus
28	18	30.0	10	2	Q8SHC3	furcifer laevis	Q8shc3 furcifer laevis
29	18	30.0	11	1	LPW_THETH	thermus thermophilus	P05624 thermus thermophilus
30	18	30.0	11	1	TRNA_SCYCA	scylliorhinus	P41333 scylliorhinus
31	18	30.0	11	2	Q9UELO	homo sapien	Q9uelo homo sapien

RESULT 1							
ID	077895	PRELIMINARY;	PRT;	11 AA.			
AC	077895;				SEQUENCE FROM N.A.		
DT	01-NOV-1998	(TREMBLrel.	08,	Created)	MEDLINE=98315113;	PubMed=9649539;	
DT	01-NOV-1998	(TREMBLrel.	08,	Last sequence update)	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,		
DT	01-DEC-2001	(TREMBLrel.	19,	Last annotation update)	Figueiro P., Sultmann H., Klein J.;		
DE					"Linkage relationships and haplotypic polymorphism among cichlid MHC genes II B loci";		
DR					Genetics 149:1527-1537(1998).		
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER	1	
FT					SEQUENCE	11 AA;	
FT					RL	1367 MW;	
FT					DR	3F47C9EA772045A3 CRC64;	
FT					EMBL; AF050005; AAC134.1; -.		
FT					NON_TER		

RA Figueiro F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT Class II loci";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050006; AAC1345..1; -.
 PT NON-TER 1 1
 FT NON-TER 11 11
 SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;
 Query Match Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
 Qy 4 FFSELW 9
 Db 3 FWSMLW 8

RESULT 3
 P92576 PRELIMINARY; PRT; 10 AA.
 ID P92576; AC 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Cytochrome c oxidase subunit I (Fragment).
 GN Name=CO1;
 OS Bipes biporus (Baja worm lizard).
 OC Mitochondrion.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
 NCBI_TaxID=52188;
 RN [1] -
 RP SEQUENCE FROM N.A.; MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 DR GO:0000739; TI13838; AA848271.1; -.
 DR PIR; TI13838; TI13838.
 DR GO:0000739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON-TER 10 10
 SQ SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;
 Query Match Score 23; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

RESULT 4
 P83537 PRELIMINARY; PRT; 11 AA.
 ID P83537; AC 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

OX NCBITaxID=1625;
 RN [1] -
 RP SEQUENCE AND INDUCTION.
 RC STRAIN=DSM 20451;
 PubMed=12112860;
 DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
 RA Drews O., Weiss W., Reil G., Parlar R., Wait R., Goerg A.;
 RT Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774 (2002).
 CC !- INDUCTION: By elevated hydrostatic pressure.
 CC !- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 protein is: 65 kDa.
 CC
 FT NON-TER 1 1
 FT SEQUENCE 11 AA; 1249 MW; D96C9231B771ADD9 CRC64;

RESULT 5
 Q95953 PRELIMINARY; PRT;
 ID Q95953; AC 095953; DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Galactocerebrosidase (EC 3.2.1.46) (Fragment).
 GN Name=GALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lulli L., Torchiana E., Finocchiaro G.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77631; ADD15626..1; -.
 DR GO:0004336; F:Galactosylceramidase activity; IEA.
 DR GO:0016798; F:Hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; F:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON-TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADC2C699C8 CRC64;

RESULT 6
 Q6LA62 PRELIMINARY; PRT;
 ID Q6LA62; AC 06LA62; DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Amiloride-sensitive epithelial sodium channel gamma subunit
 (Fragment).
 GN Name=SCNN1G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy 1 TGSFP 5
OX NCBI_TaxID=9606;	Db 5 TGSFH 9
RN [1]	
RP SEQUENCE FROM N.A. PubMed=8824247; DOI=10.1074/jbc.271.42.26062;	
RX MEDLINE=96421599; PMID=8824247; DOI=10.1074/jbc.271.42.26062;	
RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;	
RT "Genomic organization and the 5' flanking region of the gamma subunit	
RT of the human amiloride-sensitive epithelial sodium channel.";	
RL J. Biol. Chem. 271:26062-26066(1996).	
RN [2]	
RP SEQUENCE FROM N.A. PubMed=9654208;	
RX MEDLINE=98316780; PMID=9654208; DOI=10.1074/jbc.273.42.26062;	
RA Ludwig M., Bolkenius U., Wickert L., Marynen P., Bidlingmaier F.;	
RT "Structural organization of the gene encoding the alpha-subunit of the	
RT human amiloride sensitive epithelial sodium channel.";	
RL Hum. Genet. 102:576-581(1998).	
DR EMBL:292982; CAB:07506.1; -;	
DR GO:GO:0005216; F:ion channel activity; IEA.	
KW Ionic channel.	
FT NON_TER 1 1	
FT NON_TER 10 10	
SQ SEQUENCE 10 AA; 1157 MW; DBAFF83733805A2 CRC64;	
Query Match 33.3%; Score 20; DB 2; Length 10;	
Best Local Similarity 57.1%; Pred. No. 9.1e+03;	
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy 3 SPFSELW 9	
Db 1 SVVSEKW 7	
RESULT 7	
CA42_LITCI CA42_LITCI STANDARD; PRT; 11 AA.	
AC PB2052;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DE Caeruleum 4.2/4.2Y4.	
OS Litoria citropa (Australian blue mountains tree frog).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Riliidae;	
OC Peleodryadinae; Litoria.	
NCBI_TaxID=94770;	
RN [1]	
RP SEQUENCE, AND MASS SPECTROMETRY.	
RC TISSUE=Skin secretion;	
RT MEDLINE=007701; PubMed=10589099;	
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;	
RT "Caerulein-like peptides from the skin glands of the Australian blue	
RT mountains tree frog Litoria citropa. Part 1. Sequence determination	
RT using electrospray mass spectrometry.";	
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).	
CC -!- SUBCELLULAR LOCATION: Secreted.	
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.	
CC -!- MASS SPECTROMETRY: Isoform 4.2 differs from isoform 4.2 in not being sulfated.	
CC NOTE=Ref.1.	
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.	
DR InterPro; IPR001651; Gastrin.	
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.	
KW Amidation; Amphibian defense peptide; direct protein sequencing;	
KW Hypotensive agent; Pyrrolidone carboxylic acid; Sulfation.	
PT MOD_RES 1 1	
PT MOD_RES 4 4	
PT SEQUENCE 11 AA; 1344 MW; 10DAB94F5B861BB CRC64;	
Query Match 33.3%; Score 20; DB 1; Length 11;	
Best Local Similarity 80.0%; Pred. No. 1e+04;	
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 8	
CORZ_PERAM ID CORZ_PERAM STANDARD; PRT; 11 AA.	
AC P11496;	
DT 01-OCT-1989 (Rel. 12, Created)	
DT 01-FEB-1994 (Rel. 28, Last sequence update)	
DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DE Corazonin.	
OS Periplaneta americana (American cockroach).	
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Blattaria; Blattoidea;	
OC Neoptera; Orthopteroidea; Dictyoptera; Blattidae; Periplaneta.	
NCBI_TaxID=6978;	
RN [1]	
RP SEQUENCE.	
RC TISSUE=Corpora cardiaca;	
RX MEDLINE=89325572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;	
RA Veensbra J.A.;	
RT "Isolation and structure of corazonin, a cardioactive peptide from the	
RT American cockroach."	
RL FEBS Lett. 250:231-234 (1989).	
CC -!- FUNCTION: Cardioactive Peptide. Corazonin is probably involved in	
CC the physiological regulation of the heart beat.	
CC -!- SUBCELLULAR LOCATION: Secreted.	
DR PIR: S05002; S05002.	
KW Amidation; Direct protein sequencing; Neuropeptide;	
KW Pyrrolidone carboxylic acid.	
FT MOD_RES 1 1	
FT MOD_RES 11 11	
FT SEQUENCE 11 AA; 1387 MW; C7CF32D6415AB46 CRC64;	
Query Match 33.3%; Score 20; DB 1; Length 11;	
Best Local Similarity 42.4%; Pred. No. 1e+04;	
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
Qy 5 FSELTWS 11	
Db 5 YSRGWTN 11	
RESULT 9	
077894 PRELIMINARY; PRT; 11 AA.	
ID 077894	
AC 077894	
DT 01-NOV-1998 (TREMBLrel. 08, Created)	
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE MHC class II B locus 12 (Fragment).	
OS Oreochromis niloticus (Nile tilapia) (Oreochromis niloticus).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterii; Teleostei; Buteleostei; Neoteleostei;	
OC Cichlidae; Oreochromis.	
NCBI_TaxID=8128;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=98315113; PubMed=9649539;	
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,	
RA Figueredo F., Sultmann H., Klein J.;	
RT "Linkage relationships and haplotype polymorphism among cichlid MHC	
RT class II B loci."	
RL DR AF05004; AAC1341.1; -;	
FT NON_TER 1 1	
FT NON_TER 11 11	
FT SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;	

Qy	4 PFSSELW 9 : : Db	3 FWSIVW 8 .	Score 20; DB 2; Length 11; Best Local Similarity 50.0%; Pred. No. 1e+04; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Db	4 : : 4 SFWVFLFS 11
RESULT 10					
077898	ID PRELIMINARY;	PRT; 11 AA.			
AC 077898;	DT 01-NOV-1998 (TREMBLrel. 08, Created)				
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)					
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DB MHC class II B locus 12 (Fragment).					
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Teleostei; Neoteleostei; Perciformes; Labroidei; Cichlidae; Oreoichromis.					
RN [1]	SEQUENCE FROM N.A., PubMed=9649539;				
RX MEDLINE=9815113;	RA Malaga-Trillo E.; Zaleska-Rutczynska Z., McAndrew B., Vincent V., Piquero F., Sultmann H., Klein J.;				
RT "Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci.";	RT Genetics 149:1527-1537(1998).				
RL DR AF050008; AAC41347.1; -.					
FT NON_TER 1 1					
FT SEQENCE 11 AA; 1367 MW;	3F47DC0A62C045A3 CRC64;				
SQ					
Qy	4 PFSSELW 9 : : Db	3 FWSIVW 8 .	Score 20; DB 2; Length 11; Best Local Similarity 50.0%; Pred. No. 1e+04; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Db	2 GSFF 5 : 1 GNFF 4
RESULT 11					
Q65CG7	ID PRELIMINARY;	PRT; 11 AA.			
AC Q65CG7;	DT 25-OCT-2004 (TREMBLrel. 28, Created)				
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)					
DB Transcriptional activator (Fragment).					
GN Name=AC2;					
OS Sinaloa tomato leaf curl virus.					
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.					
NCBI TaxID:71186;					
RN [1] -	RP SEQUENCE FROM N.A.				
RC STRAIN=NI3;	RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in Nicaragua."				
RA Rojas A., Kvarnveden A., Rodriguez D., Valkonen J.P.T.;	RT Transcriptional activator (Fragment).				
RT DR EMBL; AJ508781; CAD48523.1; -.					
FT NON_TER 1 1	FT SEQENCE 11 AA; 1356 MW;	861BC90602D379DS CRC64;			
SQ					
Qy	4 PFSSELW 9 : : Db	3 FWSIVW 10 .	Score 20; DB 2; Length 11; Best Local Similarity 50.0%; Pred. No. 1e+04; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	Db	8 LWTS 11 : 1 MWTA 4

RESULT 14
 Q7LZZ7 PRELIMINARY; PRT; 8 AA.
 ID Q7LZZ7;
 AC ;
 DT 01-MAR-2004 (T=EMBLrel. 26, Created)
 DT 01-MAR-2004 (T=EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T=EMBLrel. 26, Last annotation update)
 DE Acetylcholinesterase (EC 3.1.1.7), venom (Fragment).
 OS Naja oxiana (Central Asian cobra) (Oxus cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=8657;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91296772; PubMed=20680931;
 RA Kreienkamp H.J., Weisse C., Raba R., Aviksaar A., Hucho F.;
 RT "Anionic subsites of the catalytic center of acetylcholinesterase from
 Torpedo and from cobra venom."
 RT Proc. Natl. Acad. Sci. U.S.A. 88:6117-6121(1991).
 RL PIR; A41117; A11117.
 DR GO:0003990; F:acetylcholinesterase activity; IEA.
 PT NON-TER 1 1
 FT 8 8
 SQ SEQUENCE 8 AA; 918 MW; 7F57645376B1DD8 CRC64;
 SEQUENCE.

Query Match Score 19; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Ov 6 SELW 9
 Db 2 AEMW 5
 :|:
 NCBI_TaxID=9913;

RESULT 15

Q9TR47 PRELIMINARY; PRT; 10 AA.
 ID Q9TR47;
 AC ;
 DT 01-MAY-2000 (T=EMBLrel. 13, Created)
 DT 01-MAY-2000 (T=EMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (T=EMBLrel. 19, Last annotation update)
 DE Amphoterin homolog (Fragment).
 OS Bos taurus (Bovine).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos
 OX NCBI_TaxID=9913;
 RP SEQUENCE.
 RX MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;
 RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
 RA Nagashima M., Lundh E.R., Vijay S., Nitzeck D.;
 RA "The receptor for advanced glycation end products (RAGE) is a cellular
 RT binding site for amphoterin. Mediation of neurite outgrowth and co-
 RT expression of rage and amphoterin in the developing nervous system.";
 RL J. Biol. Chem. 270:25752-25761(1995).
 SQ SEQUENCE 10 AA; 1163 MW; 28E5034453769B18 CRC64;
 SEQUENCE.
 Query Match Score 19; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Ov 7 ELWTS 11
 Db 4 EMWNN 8
 :|:
 NCBI_TaxID=9913;

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:07:20 ; Search time 169 Seconds (without alignments)

25.174 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFSELWTS 11

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqP1980s:*

2: geneseqP1290s:*

3: geneseqP2000s:*

4: geneseqP2001s:*

5: geneseqP2002s:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004s:*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	56.7	8	AAB09130	Aab09130 Hepatitis
2	31	51.7	10	8 ADK09671	Adk09671 Human Pap
3	31	51.7	10	8 ADK09188	Adk09188 Human Pap
4	30	50.0	6	6 ABR46515	Abr46515 Staphyloc
5	30	50.0	9	2 AAW72493	Aaw72493 Dengue vi
6	30	50.0	10	2 AAW37198	Aaw37198 Human onc
7	29	48.3	7	2 AAY33139	Aay33139 Rabbit ca
8	29	48.3	10	5 AAY93215	Aay93215 Gramnology
9	29	48.3	11	6 ABG37125	Abj37125 Rhodobin
10	28	46.7	6	6 ABR46459	Abr46459 Staphyloc
11	28	46.7	7	8 ADD68302	Adr68302 Androgen
12	28	46.7	9	2 AAY04678	Aay04678 Peptide #
13	28	46.7	10	4 ABB55959	Abb55959 Vascular
14	28	46.7	11	3 AAY93379	Aay93379 Binding m
15	28	46.7	11	7 ADF53467	Adf53467 MCPc 603
16	27	45.0	6	2 AAR89913	Aar89913 P53 /MDM2
17	27	45.0	6	2 AAW13606	Aaw13606 P53 Prote
18	27	45.0	6	3 AAB17074	Aab17074 Ndm /hdm a
19	27	45.0	6	5 ABB73169	Abb73169 Ndm /hdm a
20	27	45.0	6	6 ABR46627	Abr46627 Staphyloc
21	27	45.0	6	6 ABR46507	Abr46507 Staphyloc
22	27	45.0	6	6 ABC73432	Abc73432 Human P53
23	27	45.0	7	7 ADJ73323	Adj73323 Mdm /hdm a
24	27	45.0	6	8 ADJ52957	Adj52957 CH1 delet
25	27	45.0	6	8 ADJ51918	Adj51918 CH1 delet

ALIGNMENTS

RESULT 1	
ID	AAB09130 standard; protein; 8 AA.
XX	XX
AC	AC
XX	XX
DT	06-AUG-2003 (revised)
DT	30-AUG-2000 (first entry)
XX	XX
DE	Hepatitis GB virus protein sequence SEQ ID NO:252.
XX	XX
KW	Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection; detection; characterisation; hepatitis.
XX	OS Hepatitis GB virus.
XX	XX
PN	US6051374-A.
XX	XX
PD	18-APR-2000.
XX	XX
PP	07-JUN-1995;
PP	95US-00438445.
XX	XX
PR	14-FEB-1994;
PR	94US-00196030.
PR	13-MAY-1994;
PR	94US-0022654.
PR	29-JUL-1994;
PR	94US-00283314.
PR	23-NOV-1994;
PR	94US-00344185.
PR	23-NOV-1994;
PR	94US-00344190.
PR	30-JAN-1995;
XX	95US-00377557.
(ABBO) ABBOTT LAB.	
XX	
PI	Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI	Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX	XX
DR	WPI : 2000-338307/29.
PT	Detecting target hepatitis GB virus nucleic acid in a test sample suspected of containing HGBV comprises reacting the test sample the HGBV polynucleotide probe and detecting the complex that contains target HGBV.
PT	Example 9; Col 331-332; 369pp; English.
PS	
XX	The present invention describes a method for detecting target hepatitis GB virus (HGV) nucleic acid (RNA) in a test sample (T) suspected of containing HGBV. The method involves reacting (T) with a HGBV polynucleotide probe (I), containing 15 contiguous nucleotides, and which selectively hybridises to the HGBV genome or its full complement, and detecting the complex that contains THN, indicating the presence of

target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing agents collectively termed as hepatitis GB virus. AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and protein sequences used in the exemplification of the present invention. (Updated on 06-AUG-2003 to correct OS field.)

SQ Sequence 8 AA;

Query Match Score 34; DB 3; Length 8;

Best Local Similarity 85.7%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FSELWTS 11

| | | |

Db 1 FSHLWTS 7

OS Human papillomavirus.

XX

RESULT 2

ADK09671

ID ADK09671 standard; peptide; 10 AA.

XX

AC ADK09671;

XX

06-MAY-2004 (first entry)

XX

Human papillomavirus Peptide #1726.

XX

DE Human papillomavirus

XX

pathogenic virus; alternative reading frame; antigenic determinant;

XX

virucide; vaccine; therapeutic agent; infection; HPV.

XX

OS Human papillomavirus.

XX

PN WO2004011650-A2.

XX

PD 05-FEB-2004.

XX

PP 24-JUL-2003; 2003WO-EP008112.

XX

PR 24-JUL-2002; 2002AT-00001124.

XX

PR 11-JUL-2003; 2003EP-00450171.

XX

(INTE-) INTERCELL AG.

XX

PA Mattner F, Schmidt W, Habel A;

XX

PI Mattner F, Schmidt W, Habel A;

XX

DR WPI; 2004-169243/16.

XX

PS WPI; 2004-169243/16.

XX

RN Page 187; 220pp; English.

XX

RS This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.

XX

SQ Sequence 10 AA;

XX

PS Query Match Score 31; DB 8; Length 10;

XX

PS Best Local Similarity 51.7%; Pred. No. 96;

XX

PS Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX

PS Qy 3 SFPSLWT 10

XX

PS Db 1 SFPSLWT 8

XX

PS RESULT 4

ABR46515

ID ABR46515 standard; peptide; 6 AA.

XX

AC ABR46515;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #1705.

XX

DE CHIPs; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;

KW

Db 1 ||||| : 1 SFPSLWT 8

XX

AC ADK09188;

XX

DT 06-MAY-2004 (first entry)

XX

DB Human papillomavirus peptide #1243.

XX

DB Pathogenic virus; alternative reading frame; antigenic determinant;

XX

KW viricide; vaccine; therapeutic agent; infection; HPV.

XX

OS Human papillomavirus.

XX

PN WO2004011650-A2.

XX

PD 05-FEB-2004.

XX

PP 24-JUL-2003; 2003WO-EP008112.

XX

PR 24-JUL-2002; 2002AT-00001124.

XX

PR 11-JUL-2003; 2003EP-00450171.

XX

(INTE-) INTERCELL AG.

XX

PA Mattner F, Schmidt W, Habel A;

XX

PI Mattner F, Schmidt W, Habel A;

XX

DR WPI; 2004-169243/16.

XX

PS New polypeptide encoded by an alternative reading frame of a pathogenic

PT virus comprising an antigenic determinant, useful for treating or

PT preventing an infection with the pathogenic virus.

XX

PS Claim 18; Page 192; 220pp; English.

XX

PS This invention relates to a novel polypeptide encoded by an alternative

CC reading frame of a pathogenic virus, where the polypeptide starts with a

CC methionine amino acid residue, which comprises an antigenic determinant

CC and more than 7 amino acid residues. The invention may be useful for the

CC production of compounds with a virucide activity or the development of a

CC vaccine. The polypeptide or its fragments may be useful as a therapeutic

CC agent. It is also useful for the manufacture of a medicament for treating

CC or preventing an infection with the pathogenic virus. The present

CC sequence is that of a human papillomavirus (HPV) epitope peptide of the

CC invention.

XX

SQ Sequence 10 AA;

XX

PS Query Match Score 31; DB 8; Length 10;

XX

PS Best Local Similarity 51.7%; Pred. No. 96;

XX

PS Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX

PS Qy 3 SFPSLWT 10

XX

PS Db 1 SFPSLWT 8

XX

PS RESULT 4

ABR46515

ID ABR46515 standard; peptide; 6 AA.

XX

AC ABR46515;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #1705.

XX

DE CHIPs; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;

KW

KW

formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 inflammation; cardiovascular disease; central nervous system disease;
 gastrointestinal disease; skin disease; genitourinary disease;
 joint disease; respiratory disease; HIV infection; antiinflammatory;
 cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
 gynecological; immunosuppressive; anti-HIV
 XX OS OS
 Staphylococcus aureus.
 Synthetic.
 WO2003006048-A1.
 XX XX
 23-JAN-2003.
 PD PD
 XX XX
 11-JUL-2001; 2001WO-EP008004.
 PPF PPF
 XX XX
 11-JUL-2001; 2001WO-EP008004.
 PPR PPR
 XX XX
 (JARI-) JARI PHARM BV.
 PA PA
 Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
 Van Strijp JAG;
 WO1, 2003-256333/5.
 XX XX
 Combination of peptides derived from chemotaxis inhibiting protein from
 Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 prophylaxis and treatment of inflammation, cardiovascular, skin and
 kidney diseases.
 Disclosure; Page 17; 89pp; English.
 XX XX
 The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 -ABR4735) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 staphylococcus aureus. The peptide fragments are useful in the
 prophylaxis or treatment of diseases or disorders involving the C5a-
 receptor (C5aR) and/or formylated peptide receptor (PPR) or neutrophils,
 monocytes and endothelial cells or involving acute or chronic
 inflammation reactions. The diseases or disorders include cardiovascular
 diseases, disease of the central nervous system, gastrointestinal
 diseases, skin diseases, genitourinary diseases, joint diseases,
 respiratory diseases and HIV infection.

Sequence 6 AA;
Query Match Score 30; DB 6; Length 6;

Dengue virus -
USS824506-A.
20-OCT-1998.

XX	PF	15-AUG-1994;	94US-00290268.
XX	PR	15-AUG-1994;	94US-00290268.
XX	PA	(GENE-) GENELABS DIAGNOSTICS PTE LTD.	
XX	PI	Chan L, Guan M;	
XX	WPI	1998-582552/49.	
XX	PT	Dengue virus peptide antigens - espec	
XX	PT	infection.	
XX	PS	Example 1; Col 17; 21PP; English.	
XX	AAW72456	to AAW72570 represent peptide	
CC	type-2 Glycoprotein NS1, which was us		
CC	invention for an epitope mapping assay		
CC	peptide antigens consisting of fragment		
CC	The peptide antigens can be used for		
CC	infection by detection of antibodies		
CC	comprising attaching the antigen to a		
CC	sample with the support, and detecting		
CC	anti-human antibody or used for prepara		
CC	tion.		
XX	SQ	Sequence 9 AA;	
CC	AAW72456	Query Match 50.0%; Score 50.0%;	
CC	AAW72456	Best Local Similarity 50.0%; Pred. No	
CC	AAW72456	Matches 4; Conservative 2; Mismat	
Qy	2	GSPFSELW 9	
Db	1	:	
		1 GVEFTNIN 8	
RESULT 6			
ID	AAW37198	standard; peptide; 10 AA.	
XX	AAW37198		
AC	AAW37198;		
XX			
DT	20-JUL-1998	(first entry)	
DE	Human oncogenic protein MDM2 binding C		
XX	MDM2; oncogenic protein; p53; human; ;		
KW	tumour; diagnosis; binding; viral infec		
KW			
XX	Synthetic.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Modified-site	1	
FT		/note= "N-terminal ac	
FT		to 6-acryloyl-2-(dime	
FT	Modified-site	10	
FT		/note= "C-terminal am	
XX	W09801467-A2.		
XX	15-JAN-1998.		
PD	PF	97WO-EP003549.	
XX	XX		
PR	04-JUL-1996;	96GB-00014197.	
PR	05-JUL-1996;	97GB-00007041.	
PR	07-APR-1997;		
XX			
PA	(NOVS) NOVARTIS AG.		
PA	(CANC-) CANCER RESEARCH CAMPAIGN TECHNOLOGY		
XX	XX		

PI Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 XX DR; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 XX Example 2; Page 20; 45pp; English.

XX This is a Cys (Acrild) peptide derivative capable of binding to a human
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
 CC inhibit or block the binding of MDM2 to the human p53 protein, *in vitro*
 CC or *in vivo*. Inhibiting the interaction between the p53 and MDM2 can
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC molecules that bind to MDM2 and to identify and design inhibitors of
 especially MDM2, diagnose disease by measuring levels of MDM2 in blood, of
 cancer and leukaemia patients and for treatment or prevention of disease
 involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 CC injection. By interfering with MDM2/p53 interaction, the peptides can
 activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53
 XX Sequence 10 AA;

SQ Query Match 50.0%; Score 30; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELW 9
 :|:|||
 Db 2 GPFTFSDW 9

RESULT 7
 ID AAY333139 standard; peptide; 7 AA.
 XX AC AAY333139;
 XX DT 16-NOV-1999 (first entry)
 XX DS Rabbit carboxylesterase protein fragment #3.
 KW Carboxylesterase; rabbit; tumour cell; chemotherapy; prodrug; recurrence;
 KW disease specific promoter; CRT-11; APC; resection; recurrence;
 KW inhibition; bone marrow cell.
 OS Oryctolagus cuniculus.
 XX PA WO9942593-A1.
 XX PD 26-AUG-1999.
 XX PF 12-FEB-1999; 99WO-US003171.
 XX PR 19-FEB-1998; 98US-0075258P.
 XX PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX PI Danks MK, Potter PM, Houghton PJ;
 XX DR WPI; 1999-540311/45.
 XX PT New carboxylesterase polypeptide for treatment of tumors.
 XX PS Example 2; Page 57; 70pp; English.

CC This invention describes a novel rabbit carboxylesterase polypeptide (I)
 CC capable of metabolizing a chemotherapeutic prodrug and its inactive
 CC metabolites into an active drug. The invention also describes a
 CC composition comprising (I) and a disease-specific responsive promoter.
 CC This composition is useful for sensitizing tumor cells to a
 CC chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into
 CC tumor cells, and contacting the sensitized cells with a chemotherapeutic
 CC prodrug to inhibit growth of the tumor cells. The composition can also be
 CC administered to the site of tumor resection to inhibit tumor recurrence,
 CC and be administered to bone marrow cells to remove tumor cells. The
 CC products of the invention are useful for identifying drugs that are
 CC inactivated by a carboxylesterase enzyme, and are also useful for
 CC identifying compounds containing a COOC ester linkage that are activated
 CC by a carboxylesterase enzyme. This sequence represents a fragment of a
 CC rabbit carboxylesterase which is described in the method of the invention
 XX Sequence 7 AA;

SQ Query Match 48.3%; Score 29; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SFSSELW 9
 :|:|||
 Db 1 AFWTIELW 7

RESULT 8
 ID AAU93215 standard; peptide; 10 AA.
 XX AAU93215;
 AC AAU93215;
 XX DT 02-JUL-2002 (first entry)
 XX DE Granulocyte-colony stimulating factor receptor; cytokine;
 XX G-CSFR; granulocyte-colony stimulating factor; neutrophil proliferation; AIDS;
 KW haematopoietic growth factor; neutrophil syndrome;
 KW neutrophil differentiation; acquired immunodeficiency syndrome;
 KW chemotherapy-induced neutropenia; community acquired pneumonia;
 KW depressed neutrophil count; immunostimulant.
 XX Synthetic.
 XX OS
 XX PN WO200207676-A2.
 XX PD 31-JAN-2002.
 XX PR 20-JUL-2001; 2001WO-US023046.
 XX PR 20-JUL-2000; 2000US-00620091.
 XX PA (GLAXO) GLAXO GROUP LTD.
 XX PI Cwirla SE, Balu P, Duffin DJ, Piplani S, McEwen-Merrill B;
 PI Schatz PJ;
 XX DR WPI; 2002-329382/36.
 XX PT Novel compounds, useful for treating depressed neutrophil count, comprise
 CC peptide chains of approximately 6 to 40 amino acids in length that bind to granulocyte-
 CC colony stimulating factor receptor (G-CSFR). The compounds contain
 CC specific sequences of the generic peptides appearing as AAU9402-AAU79406
 CC and the generic sequences XV₁-XV₂-XV₃-XV₄-XV₅-XV₆-XV₇ where XV₁ =
 CC E, C, Q, V or Y; XV₂ = E, A, L, M, S, W or Q; XV₃ = K, R or T; XV₄ =
 CC L, A or V; XV₅ = R, A, M, H, E, V, L, G, D, Q or S; XV₆ = E or V; XV₇

CC = A or G; and XVII_8 = R, H, G or L) and XVI_1XVI_2XVII_3XVII_4XVII_5
 CC EXVI_6XVI_7XVI_8XVI_9 (where XVI_1 = A, E or G; XVI_2 = E, H or D; XVI_3
 CC = R or G; XVI_4 = K, Y, M, N, Q, R, D, I, S or E; XVI_5 = A, S or P;
 CC XVI_6 = E, D, T, Q, K or A; XVI_7 = R, W, K, L, S, A or Q; XVI_8 = R or E
 CC ; associated with depressed neutrophil count e.g. chemotherapy-induced
 CC neutropaenia. AIDS-induced neutropaenia or community-acquired pneumonia-
 CC induced pneumonia. The compounds are useful as *in vitro* tools for
 CC understanding the biological role of granulocyte-colony stimulating
 CC factor (G-CSF a haematopoietic growth factor and cytokine that stimulates
 CC neutrophil proliferation and differentiation), including evaluation of
 CC many factors thought to influence, and be influenced by, production of
 CC white blood cells, in the development of compounds that bind to G-CSFR,
 CC as reagents for detecting G-CSFR receptor or related receptor on living
 CC cells, fixed cells, in biological materials, *in situ* staining, fluorescence-
 CC activated cell sorting (FACS), Western blotting or enzyme-linked
 CC immunoadsorptive assay (ELISA), in receptor purification or in purifying
 CC cells expressing G-CSFR on the cell surface (or inside permeabilised
 CC cells) as a commercial research reagent for various medical and
 CC diagnostic uses or to treat a disease that would benefit from the ability
 CC to of a compound to mimic the effects of G-CSF *in vivo*. The compounds
 CC bind specifically to G-CSFR and allow for studies of biological
 CC activities mediated by the receptor and for the treatment of diseases,
 CC disorders and conditions that would benefit from activating or
 CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
 the invention

SQ Sequence 10 AA;

Query Match 48.3%; Score 29; DB 5; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SFFSEWL 9
 | : || |
 3 SFVVELW 9

RESULT 9
 ABUJ37125
 ID ABUJ37125 standard; peptide; 11 AA.
 AC ABUJ37125;
 DT 08-MAY-2003 (first entry)

XX Rhodopsin related G-protein coupled receptor binding site peptide #1.
 XX Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
 KW Rhodopsin.
 OS Unidentified.
 XX WO2003004147-A2.
 XX PD 16-JAN-2003.
 XX (BIOF-) BIOFOCUS PLC.

XX PF 05-JUL-2002; 2002WO-GB003094.
 XX PR 06-JUL-2001; 2001GB-00016570.
 XX DR WPI; 2003-221549/21.

XX Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting with
 PT ligand and motifs interacting with microenvironment, and assembling
 PT motifs.
 XX PT Disclosure; Fig 1; 39pp; English.

CC Disclosure; Fig 1; 39pp; English.
 XX

CC The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for synthesis. The
 CC novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,
 CC which relates to the novel compound library production method of the
 CC invention

SQ Sequence 11 AA;

Query Match 48.3%; Score 29; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ELWTS 11
 | || |
 2 ELWTS 6

RESULT 10

ABR46459
 ID ABR46459 standard; peptide; 6 AA.
 XX
 AC ABR46459;
 XX DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #1649.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX PN WO2003006048-A1.
 XX PD 23-JAN-2003.

XX (JARI-) JARI PHARM BV.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-De Haas CJ, Kruytzer JAW;
 PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX PS Disclosure; Page 16; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR7385) derived from the Chemoattractant Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, CC monocytes and endothelial cells or involving acute or chronic CC inflammation reactions. The diseases or disorders include cardiovascular CC diseases, disease of the central nervous system, gastrointestinal CC diseases, skin diseases, genitourinary diseases, joint diseases, CC respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match 46.7%; Score 28; DB 6; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSEELW 9 .
| : |
Db 1 FFFEW 6 .

RESULT 11
ID ADR68302 Standard; Peptide; 7 AA.

XX ADR68302;

XX 02-DEC-2004 (First entry)

DB Androgen receptor interacting peptide SEQ ID NO:20.

XX androgen receptor binding peptide; androgen receptor interacting peptide;
KW androgen receptor; cyrostatic; gene therapy; prostate cancer.

XX OS Mammalia.

OS Synthetic.

PN WO2004076473-A2.

XX PD 10-SEP-2004.

PP 10-FEB-2004; 2004WO-US003774.

XX PR 12-FEB-2003; 2003US-0446955P.

XX PA (KARO-) KARO BIO AB.

XX PI Buehrer BM, Barnett TR;

XX DR 2004-653365/63.

XX New polypeptides that bind to the androgen receptor, useful for PT diagnosis or treating diseases associated with abnormal levels of PT activation of androgen receptor, e.g. prostate cancer, or in biological PT research.

XX Disclosure; SEQ ID NO 20; 46pp; English.

XX The present invention describes a polypeptide that binds to the androgen receptor, or a polypeptide that comprises at least 50% amino acid sequence identity to the polypeptide. Also described: (1) methods of analysing the surface conformation of a protein using one or more of the polypeptide sequences mentioned above; (2) methods of identifying modulators of protein function using one or more of the polypeptide sequences mentioned above; (3) a pharmaceutical composition comprising a pharmaceutical carrier and one or more of the polypeptide sequences described above; (4) a peptide that binds to the androgen receptor, the binding being competitively inhibited by the polypeptide described above; (5) a chimeric protein comprising the above polypeptide and at least a portion of a filamentous phage protein, the portion of the filamentous phage protein being sufficient for integration of the chimeric protein into the coat of phage particles to display the polypeptide; (6) a method of filamentous phage displaying the above polypeptide; (7) a method of diagnosing a disease in a patient characterised by abnormal levels of activation of androgen receptor, comprising providing a sample of body

CC fluid or tissue of the patient, administering a diagnostic amount of the pharmaceutical composition described above, and assaying the amount of CC administered androgen receptor in the body fluid or tissue of the patient; CC and (8) a method of treating a patient suffering from a disease characterised by abnormal levels of activation of androgen receptor, comprising administering to the patient a therapeutic amount of the pharmaceutical composition described above, the androgen receptor, CC interacting polypeptide has cytostatic activity, and can be used in gene CC therapy. The composition and methods are useful for diagnosing or CC treating patients suffering from diseases characterised by abnormal CC levels of activation of androgen receptor, such as prostate cancer. They CC may also be used in biological research, as therapeutics or for in vitro CC or in vivo classification of compounds. The present sequence represents CC an androgen receptor interacting peptide, which is used in the gene exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX SQ Sequence 7 AA;

Query Match 46.7%; Score 28; DB 8; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELW 9 .
| : || |
Db 1 SRPAELW 7 .

XX
PF 16-APR-2003; 2003WO-US011935.
XX
PR 17-APR-2002; 2002US-0373686P.
XX
(CREA/) CREA R.
PA (CAPP/) CAPPUCILLI G.
XX
PI Crea R, Cappuccilli G;
XX
DR WPI: 2003-854132/79.
XX
PT Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
PT for producing mutant polypeptides comprising synthesizing oligonucleotides
PT comprising a nucleotide sequence for each target region of a prototype
PT amino acid.
XX
PS Example; Fig 7; 4 opp; English.
XX
CC This invention relates to a novel method of walk-through mutagenesis of a
CC nucleic acid encoding a polypeptide which comprises synthesising a
CC mixture of oligonucleotides comprising a nucleotide sequence for each
CC target region of a prototype amino acid, where each oligonucleotide
CC contains, at each sequence position in the target region, a prototype
CC nucleotide for synthesis of the prototype amino acid, or a predetermined
CC nucleotide that is required for synthesis of the predetermined amino
CC acid. The method is useful in producing mutant polypeptides in which the
CC overall presence of the predetermined amino acid is limited to one or two
CC positions per mutated polypeptide, leaving the remaining amino acids in
CC the targeted region intact or as close as possible to the prototype
CC sequence. The invention was exemplified using the three complementarity
CC determining regions (CDRS) of the heavy chain of the monoclonal antibody
CC MCPC 603.
XX
SQ Sequence 11 AA;
Query Match 46.7%; Score 28; DB 70; Length 11;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 3 S P F F S E L W T S 11
Db 1 S Y S S S W N S 9

Search completed: April 27, 2005, 15:26:49
Job time : 172 secs

Copyright GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:23:03 ; Search time 42 Seconds
(without alignments)

19.551 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFSELWTS 11

Scoring table: BL0SM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries
Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pop:
6: /cgn2_6/prodata/1/iaa/backfile1.pop:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	ID	Description
1	34	56.7	8	4	US-08-469-260A-252	Sequence 252, Appli	Sequence 252, Appli
2	34	56.7	8	4	US-08-488-446-252	Sequence 252, Appli	Sequence 252, Appli
3	34	56.7	8	4	US-08-467-344A-252	Sequence 252, Appli	Sequence 252, Appli
4	34	56.7	8	4	US-08-424-550B-252	Sequence 252, Appli	Sequence 252, Appli
5	30	50.0	6	1	US-08-424-957-6	Sequence 6, Appli	Sequence 6, Appli
6	30	50.0	6	3	US-09-035-686-6	Sequence 6, Appli	Sequence 6, Appli
7	30	50.0	11	1	US-08-424-957-42	Sequence 42, Appli	Sequence 42, Appli
8	30	50.0	11	3	US-09-035-688-42	Sequence 42, Appli	Sequence 42, Appli
9	29	48.3	7	4	US-09-595-602B-10	Sequence 10, Appli	Sequence 10, Appli
10	29	48.3	10	4	US-09-620-091-28	Sequence 28, Appli	Sequence 28, Appli
11	28	46.7	11	3	US-09-186-955-6	Sequence 6, Appli	Sequence 6, Appli
12	28	46.7	11	3	US-09-669-271A-6	Sequence 6, Appli	Sequence 6, Appli
13	28	46.7	11	4	US-09-881-276-6	Sequence 6, Appli	Sequence 6, Appli
14	27	45.0	6	1	US-08-277-660A-2	Sequence 2, Appli	Sequence 2, Appli
15	27	45.0	6	1	US-08-424-957-2	Sequence 2, Appli	Sequence 2, Appli
16	27	45.0	6	3	US-09-035-686-2	Sequence 2, Appli	Sequence 2, Appli
17	27	45.0	6	4	US-09-081-975-1	Sequence 1, Appli	Sequence 1, Appli
18	27	45.0	6	4	US-09-028-002B-130	Sequence 130, Appli	Sequence 130, Appli
19	27	45.0	6	4	US-09-732-384-4	Sequence 4, Appli	Sequence 4, Appli
20	27	45.0	7	1	US-08-277-660A-27	Sequence 27, Appli	Sequence 27, Appli
21	27	45.0	7	1	US-08-424-957-15	Sequence 15, Appli	Sequence 15, Appli
22	27	45.0	7	1	US-08-424-957-19	Sequence 19, Appli	Sequence 19, Appli
23	27	45.0	7	3	US-09-035-686-15	Sequence 15, Appli	Sequence 15, Appli
24	27	45.0	7	3	US-09-035-686-19	Sequence 19, Appli	Sequence 19, Appli
25	27	45.0	10	1	US-08-277-660A-7	Sequence 7, Appli	Sequence 7, Appli
26	27	45.0	10	1	US-08-424-957-11	Sequence 11, Appli	Sequence 11, Appli
27	45.0	10	1	US-08-424-957-17	Sequence 18, Appli	Sequence 18, Appli	

ALIGNMENTS

RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6515178

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOF
APPLICANT: JAMES C. ERICK
APPLICANT: SHERI L. BULJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-469-260A-252
 Query Match 56.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy ||| | | |
 Db 1 FSHLWTS 7

RESULT 2
 US-08-488-446-252
 ; Sequence 252, Application US/08488446
 GENERAL INFORMATION:
 ; Parent No. 6588898
 ; NUMBER OF SEQUENCES: 716
 ; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 716
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 ; STREET: 100 ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,344A
 ; FILING DATE: 07-Jun-1995
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/424,550
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FOREMBSK, PRISCILLA E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-938-2623
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
 ; US-08-467-344A-252

Query Match 56.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy ||| | | |
 Db 1 FSHLWTS 7

RESULT 3
 US-08-488-446-252
 Query Match 56.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 FSELWTS 11
 Db 1 FSHLWTS 7

US-08-467-344A-252
 ; Sequence 252, Application US/08467344A
 ; Patent No. 6596559
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; TAMI J. PILOT-MATIAS
 ; GEORGE J. DAWSON
 ; SURESH M. DESAI
 ; THOMAS P. LEARY
 ; ANTHONY SCOTT MUERHOFF
 ; JAMES C. ERKER
 ; SHERI L. BUIJK
 ; ISA K. MUSHAWAR
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 ; NUMBER OF SEQUENCES: 716
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 ; STREET: 100 ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,344A
 ; FILING DATE: 07-Jun-1995
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/424,550
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FOREMBSK, PRISCILLA E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-938-2623
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
 ; US-08-467-344A-252

Query Match 56.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 FSELWTS 11
 Db 1 FSHLWTS 7

RESULT 4
 US-08-424-550B-252
 ; Sequence 252, Application US/08424550B
 ; Patent No. 6720166
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; TAMI J. PILOT-MATIAS
 ; GEORGE J. DAWSON
 ; SURESH M. DESAI
 ; THOMAS P. LEARY
 ; ANTHONY SCOTT MUERHOFF
 ; APPLICANT:

APPLICANT: JAMES C. ERKER
 APPLICANT: SHERIL L. BUIK
 APPLICANT: ISA K. MUSHARWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 ZIP: 60064-3500
 COUNTRY: USA
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550B
 FILING DATE:
 CLASSIFICATION: 435435
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-424-550B-252

Query Match, Score 56.7%; Pred. No. 4.1e+05; Length 8;
 Best Local Similarity 85.7%; 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FSELWTS 11
 | | ||| 1
 Db 1 FSHLWTS 7

RESULT 5
 US-08-424-957-6
 Sequence 6, Application US/08424957
 Patient No. 5770377
 GENERAL INFORMATION:
 APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,686

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/424,957
 FILING DATE: 19-APR-1995
 APPLICATION NUMBER: US 08/277,660
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,686

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown

US-09-035-686-6

Query Match Similarity Score 30; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9
 Db 2 FSBLW 6

RESULT 7
 US-08-424-957-42
 ; Sequence 42, Application US/08424957

; GENERAL INFORMATION:
 ; APPLICANT: Picklesley, Steven M.
 ; ATTORNEY: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; CITY: Four Embarcadero Center, Suite 3400
 ; STATE: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown

US-09-035-686-42

Query Match Similarity Score 30; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9
 Db 5 FSBLW 9

RESULT 9
 US-09-595-682B-10
 ; Sequence 10, Application US/09595682B

; GENERAL INFORMATION:
 ; APPLICANT: Danks, Mary K.
 ; ATTORNEY: Potter, Philip M.
 ; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tumor Cells
 ; FILE REFERENCE: SU-0005
 ; CURRENT APPLICATION NUMBER: US/09/595,682B
 ; CURRENT FILING DATE: 2000-01-16
 ; PRIOR APPLICATION NUMBER: 60/075,258
 ; PRIOR FILING DATE: 1998-02-19
 ; PRIOR APPLICATION NUMBER: PCT/US99/03171
 ; PRIOR FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SEQ ID NO 10
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-09-595-682B-10

Query Match Similarity Score 30; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9
 Db 5 FSBLW 9

RESULT 8
 US-09-035-686-42
 ; Sequence 42, Application US/09035686

; GENERAL INFORMATION:
 ; APPLICANT: Picklesley, Steven M.
 ; ATTORNEY: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

Query Match Similarity Score 29; DB 4; Length 7;

Best Local Similarity 57.1%; Pred. No. 4.1e+05;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO 6

Qy :|||
 Db 1 AFWTELM 7

RESULT 10
 US-09-620-091-28

; Sequence 28, Application US/09620091
 ; Patent No. 6716811
 ; GENERAL INFORMATION:
 ; APPLICANT: CWIRLA, STEVEN E.
 ; APPLICANT: BALU, PALANI
 ; APPLICANT: DUFFIN, DAVID J.
 ; APPLICANT: PIPLANI, SUNILA
 ; APPLICANT: MERRILL, BARBARA MCBOWEN
 ; APPLICANT: SCHATTZ, PETER JOSEPH
 ; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
 ; STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 0300-0014
 ; CURRENT APPLICATION NUMBER: US/09/620,091
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 491
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 28

; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-09-620-091-28
 Query Match 48.3%; Score 29; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO 6

Qy :|||
 Db 3 SFWVELW 9

RESULT 11
 US-09-186-958-6

; Sequence 6, Application US/09186958B
 ; Patent No. 6238860
 ; GENERAL INFORMATION:
 ; APPLICANT: Whelihan, E. Fayelle
 ; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 ; FILE REFERENCE: Dyax-009.0 US sequence listing
 ; CURRENT APPLICATION NUMBER: US/09/186,958B
 ; CURRENT FILING DATE: 1998-11-05
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide

US-09-186-958-6
 Query Match 46.7%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 SEQ ID NO 6

Qy :|||
 Db 4 PPSELWTS 11

RESULT 12
 US-09-669-271A-6

; Sequence 6, Application US/09669271A
 ; Patent No. 6291197
 ; GENERAL INFORMATION:
 ; APPLICANT: Whelihan, E. Fayelle
 ; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 ; FILE REFERENCE: Dyax-009.0 US sequence listing
 ; CURRENT APPLICATION NUMBER: US/09/669,271A
 ; CURRENT FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: 09/186,958
 ; PRIOR FILING DATE: 1998-11-05
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide

US-09-669-271A-6
 Query Match 46.7%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 SEQ ID NO 6

Qy :|||
 Db 1 FFCAEWPS 8

RESULT 13
 US-09-881-276-6

; Sequence 6, Application US/09881276
 ; Patent No. 6479611
 ; GENERAL INFORMATION:
 ; APPLICANT: Whelihan, E. Fayelle
 ; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 ; FILE REFERENCE: DYX-009.0 US-2
 ; CURRENT APPLICATION NUMBER: US/09/881,276
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 09/669,271
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Microsoft Word 97
 ; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide

US-09-881-276-6
 Query Match 46.7%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 SEQ ID NO 6

Qy :|||
 Db 1 FFCAEWPS 8

RESULT 14
 US-09-277-660A-2

; Sequence 2, Application US/09277660A
 ; Patent No. 5702908
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.

APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53 Protein and Therapeutic Application Thereof
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-60244/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1389
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-277-660A-2

Query Match Score 27; DB 1; Length 6;
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 5 FSBLW 9
 | : |
 Db 2 FSDLW 6

RESULT 15
 US-08-424-957-2
 / Sequence 2, Application US/08424957
 / Patent No. 5770377
 / GENERAL INFORMATION:
 / APPLICANT: Pickleley, Steven M.
 / APPLICANT: Lane, David P.
 / TITLE OF INVENTION: Interruption of Binding of MDM2 and P53 Protein and Therapeutic Application Thereof
 / NUMBER OF SEQUENCES: 50
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
 / STREET: Four Embarcadero Center, Suite 3400
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: United States
 / ZIP: 94111-4187
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/424,957
 / FILING DATE: 19-APR-1995
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/277,660

;/ FILING DATE: 20-JUL-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Dreger, Walter H.
 / REGISTRATION NUMBER: 24,190
 / REFERENCE/DOCKET NUMBER: A-61228/WHD
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 781-1389
 / TELEFAX: (415) 398-3249
 / TELELEX: 910 277299
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 6 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: unknown
 / US-08-424-957-2
 Query Match Score 27; DB 1; Length 6;
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 5 FSBLW 9
 | : |
 Db 2 FSDLW 6

Search completed: April 27, 2005, 15:31:20
 Job time : 44 secs

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OM protein - protein search, using SW model

Run on: April 27, 2005, 15:29:56 ; Search time 130 Seconds (without alignments)

Scoring table: BLOSUM62

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFSELWTS 11

Scoring table: GapOp 10.0 , Gapext 0.5

Searched: 142401 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 197300

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/picodata/2/pubpaa/us06_NEW_PUB.pep:*

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6: /cgn2_6/picodata/2/pubpaa/us09_PUBCOMB.pep:*

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10: /cgn2_6/picodata/2/pubpaa/us09C_PUBCOMB.pep:*

11: /cgn2_6/picodata/2/pubpaa/us09C_NEW_PUB.pep:*

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17: /cgn2_6/picodata/2/pubpaa/us10_NEW_PUB.pep:*

18: /cgn2_6/picodata/2/pubpaa/us11_NEW_PUB.pep:*

19: /cgn2_6/picodata/2/pubpaa/us60_NEW_PUB.pep:*

20: /cgn2_6/picodata/2/pubpaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	56.7	8	US-08-424-550B-252	Sequence 252, App1
2	30	50.0	10	9 US-09-214-371-35	Sequence 35, App1
3	30	50.0	10	9 US-09-214-371-36	Sequence 36, App1
4	29	48.3	10	17 US-10-659-207-28	Sequence 28, App1
5	28	46.7	9	9 US-09-886-724A-35	Sequence 35, App1
6	28	46.7	11	9 US-09-881-276-6	Sequence 6, App1
7	28	46.7	11	15 US-10-417-95A-56	Sequence 56, App1
8	27	45.0	6	9 US-09-214-371-83	Sequence 83, App1
9	27	45.0	6	9 US-09-732-384-4	Sequence 4, App1
10	27	45.0	6	13 US-10-155-059-1	Sequence 1, App1
11	27	45.0	6	15 US-10-609-217-110	Sequence 130, App1
12	27	45.0	6	15 US-10-632-388-130	Sequence 130, App1
13	27	45.0	6	15 US-10-651-723-130	Sequence 130, App1

ALIGNMENTS

RESULT US-08-424-550B-252

/ Sequence 252, Application US/08424550B
 / Publication No. US20020119447A1
 / GENERAL INFORMATION:
 / APPLICANT: JOHN N. SIMONS
 / APPLICANT: TAMMI J. PILOT-MATIAS
 / APPLICANT: GEORGE J. DAWSON
 / APPLICANT: GEORGE G. SCHLAUDER
 / APPLICANT: SHREESH M. DESAI
 / APPLICANT: THOMAS P. LEARY
 / APPLICANT: ANTHONY SCOTT MUEHRHOFF
 / APPLICANT: JAMES C. ERICK
 / APPLICANT: SHERI L. BULJK
 / APPLICANT: ISA K. MUSHAHWAR
 / TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 / TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 / NUMBER OF SEQUENCES: 716
 / CORRESPONDENCE ADDRESS:
 / ADDRESSE: ABBOTT LABORATORIES D377/AP6D
 / STREET: 100 ABBOTT PARK ROAD
 / CITY: ABBOTT PARK
 / STATE: IL
 / COUNTRY: USA
 / ZIP: 60064-3500
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/424,550B
 / FILING DATE:
 / CLASSIFICATION: 435435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: FOREWSKI, PRISCILLA E.

```

REGISTRATION NUMBER: 33,207
REDOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-338-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-252

Query Match      56.7%;  Score 34;  DB 8;  Length 8;
Best Local Similarity 85.7%;  Pred. No. 1.3e+06;  Mismatches 1;  Indels 0;  Gaps 0;
Db      5 FSBLWTS 11
Db      1 FSHLWTS 7

RESULT 2
US-09-214-371-35
Sequence 35, Application US/09214371B
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pickasley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
PRIORITY APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 36
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Ac-Cys
NAME/KEY: VARIANT
LOCATION: (10)
OTHER INFORMATION: x = Pro-NH2
US-09-214-371-36

Query Match      50.0%;  Score 30;  DB 9;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1.5e+02;
Mismatches 1;  Indels 2;  Gaps 0;
Db      2 GSFFSELW 9
Db      2 GPTFSDLW 9

RESULT 4
US-10-659-207-28
Sequence 28, Application US/10659207
Publication No. US200503759A1
GENERAL INFORMATION:
APPLICANT: CWIRKA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: PIPALANI, SUNIL A.
APPLICANT: MERRILL, BARBARA MCEOWEN
APPLICANT: SCHAVIT, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
OTHER INFORMATION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: USES
FILE REFERENCE: 0300-014
CURRENT APPLICATION NUMBER: US/10/659,207
PRIORITY APPLICATION NUMBER: US/09/620,091
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-10-659-207-28

Query Match      48.3%;  Score 29;  DB 17;  Length 10;
Best Local Similarity 71.4%;  Pred. No. 2.3e+02;
Mismatches 1;  Indels 0;  Gaps 0;
Db      3 SFFSELW 9
Db      1 ||| ||||

RESULT 3
US-09-214-371-36
Sequence 36, Application US/09214371B
GENERAL INFORMATION:
Patent No. US01001851A1
APPLICANT: Lane, David
APPLICANT: Bottger, Volker

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Db 3 SFWVELW 9

RESULT 5
 US-09-486-734A-35
 ; Sequence 35, Application US/09486734A
 ; Patent No. US20020164732A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chopin, Marie-Christine
 ; Clier, Florence
 ; Erlich, S.
 ; Dusko
 ; Gautier, Michel
 ; Schouler, Catherine
 ; Institut National de la Recherche Agronomique
 ; TITLE OF INVENTION: Resistance Mechanisms to IC Type R/M
 ; FILE REFERENCE: 313339/196048
 ; CURRENT APPLICATION NUMBER: US/09/485,734A
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: PCT/FR98/01873
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR FILING NUMBER: FR 97/10885
 ; OTHER INFORMATION: Hs6S subunit
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 35
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hs6S subunit
 ; SEQ ID NO: 35

Query Match 2 GSFFSEL 8
 Best Local Similarity 46.7%; Score 28; DB 9; Length 9;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 2 GSFFKQL 8
 Best Local Similarity 46.7%; Score 28; DB 9; Length 9;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
 US-09-881-276-6
 ; Sequence 6, Application US/09881276
 ; Patent No. US20020031761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Whelan, E. Payelle
 ; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 ; FILE REFERENCE: DXY-009.0 US-2
 ; CURRENT APPLICATION NUMBER: US/09/881,276
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: 09/669,271
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: 09/186,958
 ; PRIOR FILING DATE: 1998-11-05
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Microsoft Word 97
 ; SEQ ID NO: 6
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide

Query Match 4 FFSELWTS 11
 Best Local Similarity 46.7%; Score 28; DB 9; Length 11;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Query Match 5 FSELW 9
 Best Local Similarity 45.0%; Score 27; DB 9; Length 6;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Query Match 5 FSELWTS 11
 Best Local Similarity 46.7%; Score 28; DB 9; Length 11;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Query Match 5 FSELW 9
 Best Local Similarity 40.0%; Score 27; DB 9; Length 6;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-10-417-895A-56
 ; Sequence 56, Application US/10417895A
 ; Publication No. US2004033569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cre, Roberto
 ; APPLICANT: Capuccilli, Guido
 ; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
 ; FILE REFERENCE: 1551-DOP02-001
 ; CURRENT APPLICATION NUMBER: US/10/417,895A
 ; CURRENT FILING DATE: 2003-04-16
 ; PRIOR APPLICATION NUMBER: 60/373,686
 ; PRIOR FILING DATE: 2002-04-17
 ; NUMBER OF SEQ ID NOS: 86
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 56
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: variant peptide for third complementarity
 ; OTHER INFORMATION: determining region of Fv region of an
 ; OTHER INFORMATION: immunoglobulin
 ; SEQ ID NO: 56

Query Match 3 SPFSELWTS 11
 Best Local Similarity 46.7%; Score 28; DB 15; Length 11;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Query Match 3 SPFSELWTS 11
 Best Local Similarity 44.4%; Score 28; DB 15; Length 11;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Query Match 1 SYSSSSWSS 9
 Best Local Similarity 46.7%; Score 28; DB 15; Length 11;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 US-09-214-371-83
 ; Sequence 83, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Botteger, Volker
 ; APPLICANT: Botteger, Angelica
 ; APPLICANT: Pickaley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echaverria, Carlos
 ; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
 ; FILE REFERENCE: 4-2037/A,PCT
 ; CURRENT APPLICATION NUMBER: US/09/214,371B
 ; CURRENT FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549
 ; PRIOR FILING DATE: 1997-07-04
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO: 83
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: peptide, amino acid residues 18-23 of human p53
 ; SEQ ID NO: 83

Query Match 4 FFSELWTS 11
 Best Local Similarity 45.0%; Score 27; DB 9; Length 6;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 US-09-732-384-4
 Sequence 4, Application US/09732384
 GENERAL INFORMATION:
 APPLICANT: Gu, Jijie
 TITLE OF INVENTION: Inhibition of p53 Degradation
 FILE REFERENCE: 21508-044
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: 60/169,816
 PRIOR FILING DATE: 1999-12-08
 NUMBER OF SEQ ID NOS: 10
 SEQ ID NO: 4
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence:Protein
 OTHER INFORMATION: Fragment not in inhibitory p53 polypeptide
 US-09-732-384-4

Query Match 45.0%; Score 27; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9
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 Db 2 FSDLW 6

RESULT 10
 US-10-155-059-1
 Sequence 1, Application US/10155059
 GENERAL INFORMATION:
 APPLICANT: Kaelin, William
 Jost, Christine
 TITLE OF INVENTION: METHODS OF TREATMENT USING
 NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon Peabody LLP
 STREET: 101 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/155,059
 FILING DATE: 24-May-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/081,975
 FILING DATE: 12-MAY-1998
 APPLICATION NUMBER: 60/046,207
 FILING DATE: 12-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 REFERENCE/DOCKET NUMBER: 47400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054

RESULT 11
 US-10-609-217-130
 Sequence 130, Application US/10609217
 Publication No. US20040044188A1
 GENERAL INFORMATION:
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: FEIGE, ULRICH
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/609,217
 PRIORITY APPLICATION NUMBER: US/09/428, 082B
 PRIORITY FILING DATE: 1999-10-22
 PRIORITY APPLICATION NUMBER: 60/105,371
 PRIORITY FILING DATE: 1999-10-23
 NUMBER OF SEQ ID NOS: 1133
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 130
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
 US-10-609-217-130

Query Match 45.0%; Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy ~ 5 FSBLW 9
 |:|
 Db 2 FSDLW 6

RESULT 12
 US-10-632-388-130
 Sequence 130, Application US/10632388
 Publication No. US20040053845A1
 GENERAL INFORMATION:
 APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/632,388
 PRIORITY APPLICATION NUMBER: US/09/428, 082B
 PRIORITY FILING DATE: 1999-10-22
 PRIORITY APPLICATION NUMBER: 60/105,371
 PRIORITY FILING DATE: 1998-10-23
 PRIORITY FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 130
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
 US-10-632-188-130

Query Match Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FSEIW 9
 Db 2 FSDLW 6

RESULT 13
 US-10-651-723-110
 Publication No. US20040057953A1
 GENERAL INFORMATION:
 APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/651,723
 CURRENT FILING DATE: 2003-08-29
 PRIOR APPLICATION NUMBER: US/09/428,082B
 PRIOR FILING DATE: 1999-10-22
 PRIOR APPLICATION NUMBER: 60/105,371
 PRIOR FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 1133
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 130
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
 US-10-651-723-110

Query Match Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FSEIW 9
 Db 2 FSDLW 6

RESULT 14
 US-10-645-761-130
 Publication No. US20040071712A1
 GENERAL INFORMATION:
 APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/645,761
 CURRENT FILING DATE: 2003-08-18
 PRIOR APPLICATION NUMBER: US/09/428,082B
 PRIOR FILING DATE: 1999-10-22
 PRIOR APPLICATION NUMBER: 60/105,371
 PRIOR FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 1133

RESULT 15
 US-10-666-696-130
 ; Sequence 130, Application US/10666696
 ; Publication No. US20040077022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: CHEETHAM, JANET C.
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; APPLICANT: GUDAS, JEAN MARIE
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527A
 ; CURRENT APPLICATION NUMBER: US/10/666,696
 ; CURRENT FILING DATE: 2003-09-19
 ; PRIOR APPLICATION NUMBER: US/09/563,286C
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/428,082
 ; PRIOR FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 1157
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 130
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Mdm/hdm antagonist peptide
 US-10-666-696-130

Query Match Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FSEIW 9
 Db 2 FSDLW 6

Search completed: April 27, 2005, 15:42:33
 Job time : 131 sec_B

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:30:37 ; Search time 43 Seconds
(without alignments)

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFFSELWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	44.8	10	2 C39191	hypothetical protein
2	28	41.8	9	2 S36850	Ig heavy chain V region
3	25	37.3	12	2 PT0274	Ig heavy chain CRD
4	24	35.8	7	2 PH1602	Ig H chain V-D-I r
5	22	32.8	9	2 G11946	T-cell receptor ga
6	20	29.9	6	2 B34835	dnaA protein - Pse
7	20	29.9	10	2 T13838	cytochrome-c oxidase
8	20	29.9	11	2 S05002	corazonin - American
9	19	28.4	5	2 B61445	Leu-enkephalin - b
10	19	28.4	5	2 A61445	Met-enkephalin - b
11	19	28.4	6	2 PT0519	T-cell receptor beta
12	19	28.4	6	2 A43129	neuropeptide GFR
13	19	28.4	7	2 A60224	Met-enkephalin-Arg
14	19	28.4	8	2 A41117	acytelycholinesterase
15	19	28.4	10	2 A60410	beta-neoendorphin
16	19	28.4	11	2 PT0520	Ig heavy chain CRD
17	19	28.4	12	2 I58273	thyroglobulin - rat
18	18	26.9	9	2 S07241	litorin - Bohde's
19	18	26.9	10	2 C41946	T-cell receptor ga
20	18	26.9	10	2 S53789	neuropeptide Pec-H
21	18	26.9	11	1 LEFTWE	probable trpG lea
22	18	26.9	11	1 S41147	chaperonin 10 homo
23	18	26.9	11	2 S33300	probable substance
24	18	26.9	12	2 S25056	Ig heavy chain - m
25	18	26.9	12	2 157678	gene rPLP-A protein
26	18	26.9	12	2 PH1459	T-cell receptor beta
27	17.5	26.1	8	2 JS0315	leucokinin V - Mad
28	17	25.4	7	2 PT0586	T-cell receptor beta
29	17	25.4	8	2 A44960	neuropeptide Led-C

ALIGNMENTS

RESULT 1

C39191 hypothetical protein 1 (Tetx 5' region) - *Bacteroides fragilis*

C;Species: *Bacteroides fragilis*

C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993

C;Accession: C39191

R;Speer, B. S.; Bedzyk, L.; Salyers, A. A.

J. Bacteriol. 173, 176-183, 1991

A;Title: Evidence that a novel tetracycline resistance gene found on two *Bacteroides* tr:

A;Reference number: A39191; PMID:9100280; PMID:1846135

A;Accession: C39191

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <SPB>

A;Cross-references: GB:M37699

Query Match Score 44.8%; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Gaps 0;

Qy 5 FFSEELNTS 12
Db 2 YFSRPPWTS 9

RESULT 2

S36850 Ig heavy chain V region - mouse

C;Species: *Mus musculus* (house mouse)

C;Accession: S36850

R;Jacob, J.; Kalsbeek, G.

Submitted to the EMBL Data Library, July 1992

A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl

A;Reference number: S25024

A;Accession: S36850

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-9 <JAC>

A;Cross-references: EMBL:X67387; NID:950113; PID:CAA47799_1; PID:e51594; PID:91333871

C;Keywords: heterotetramer; immunoglobulin

Query Match Score 41.7%; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYGSFF 6
Db 4 DYGSYF 9

RESULT 3

PT0274
 19 heavy chain CRD3 region (clone 3-109B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0274
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J.-Exp. Med., 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A;Reference number: PMID:1899102
 A;Accession: PT0274
 A;Molecule type: DNA
 A;Residues: 1-12 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match Similarity 37.3%; Score 25; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
 Db 3 YSSSWI 9

RESULT 4
 PH1602
 19 H chain V-D-J region (wild-type clone 313) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1602
 R;Levinson, D.A.; Canopus-Torres, J.; Ledcr, P.
 J. Exp. Med., 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PMID:815380; MUID:93301609; PMID:8315387
 A;Accession: PH1602
 A;Molecule type: DNA
 A;Residues: 1-7 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match Similarity 35.8%; Score 24; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 SELWT 11
 Db 3 SSIWLT 7

RESULT 5
 G41946
 T-cell receptor gamma chain (2t.23) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C;Accession: G41946
 R;Whetsell, M.L.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol., 11, 5902-5909, 1991
 A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
 A;Reference number: A41946; MUID:92049316; PMID:1558619
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-9 <WHE>
 C;Keywords: T-cell receptor

Query Match Similarity 32.8%; Score 22; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
 Db 2 YGSYSS 7

RESULT 6
 B34835
 dnaA protein - *Pseudomonas aeruginosa* (fragment)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 C;Accession: B34835
 R;Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A., 87, 1278-1282, 1990
 A;Title: *Pseudomonas* chromosomal replication origins: a bacterial class distinct from Escherichia coli
 A;Reference number: A34835; MUID:30160310; PMID:2106132
 A;Accession: B34835
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <HRE>
 A;Cross-references: GB:M0125; PID:9151419; PID:9151421
 C;Keywords: DNA binding

Query Match Similarity 29.9%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 BLW 10
 Db 4 BLW 6

RESULT 7
 T13838
 cytochrome-c oxidase (EC 1.9.3.1) chain I - *Bipes biporus* mitochondrion (fragment)
 C;Species: mitochondrion *Bipes biporus* (fragment)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T13838
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Pang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol., 14, 91-104, 1997
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A;Reference number: Z17789; MUID:9715326; PMID:900757
 A;Accession: T13838
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-10 <AAC>
 A;Cross-references: UNIPROT:P922576; EMBL:U71335; NID:91753232; PID:91753235; PID:AA8482
 C;Genetics:
 A;Genome: mitochondrion
 A;Note: COI
 C;Keywords: mitochondrion; oxidoreductase

Query Match Similarity 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFES 7
 Db 6 SFES 9

RESULT 8
 S05002
 corazonin - American cockroach
 C;Species: Periplaneta americana (American cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
 C;Accession: S05002
 R;Veenstra, J.A.
 FEBS Lett., 250, 231-234, 1989
 A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american cockroach
 A;Reference number: S05002; MUID:8932572; PMID:2753132
 A;Accession: S05002
 A;Molecule type: protein
 A;Residues: 1-11 <WEE>
 A;Cross-references: UNIPROT:P11496
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid (Gln) #status experimental
 F;1;Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;1;Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.0%; Pred. No. 2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy :|: 6 PSBLWTS 12
 Db 5 YSRGWTN 11

RESULT 9
 B61445 Leu-enkephalin - blue mussel
 C;Species: Mytilus edulis (blue mussel)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
 R;Leung, M.K.; Stefanoff, G.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
 A;Title: Isolation and identification of enkephalins in pedal ganglia of *Mytilus edulis*
 A;Reference number: A61445; MUID:84144823; PMID:6583690
 A;Accession: B61445
 A;Molecule type: protein
 A;Residues: 1-5 <LEU>
 A;Experimental source: pedal ganglia
 C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy :|: 2 YGSP 5
 Db 1 YGGF 4

RESULT 10
 A61445 Met-enkephalin - blue mussel
 C;Species: Mytilus edulis (blue mussel)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
 R;Leung, M.K.; Stefanoff, G.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
 A;Title: Isolation and identification of enkephalins in pedal ganglia of *Mytilus edulis*
 A;Reference number: A61445; MUID:84144823; PMID:6583690
 A;Molecule type: protein
 A;Residues: 1-5 <LEU>
 A;Experimental source: pedal ganglia
 C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy :|: 2 YGSP 5
 Db 1 YGGF 4

RESULT 11
 PTO519 T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PTO519
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PTO509; MUID:91277601; PMID:1711558
 A;Accession: PTO519
 A;Status: translation not shown
 A;Molecule type: mRNA

A;Residues: 1-6 <PFF>
 A;Experimental source: adult thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 28.4%; Score 19; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 SELW 10
 Db 2 SSILW 5

RESULT 12
 A43129 neuropeptide GNPFamide - tapeworm (*Moniezia expansa*)
 C;Species: Moniezia expansa
 C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
 C;Accession: A43129
 R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.
 Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
 A;Title: GNPFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t.
 A;Reference number: A43129; MUID:93312289; PMID:8323531
 A;Accession: A43129
 A;Molecule type: protein
 A;Cross-references: UNIPROT:P41966
 A;Keywords: amidated carboxyl end; neuropeptide
 F;Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GSFF 6
 Db 1 GNFF 4

RESULT 13
 A60224 Met-enkephalin-Arg-Phe - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
 C;Accession: A60224
 R;Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Nakk, G.; Weber, E.
 J. Neurochem. 56, 1914-1920, 1991
 A;Title: Isolation and characterisation of opioid peptides from rabbit cerebellum.
 A;Reference number: A60224; MUID:91225580; PMID:2027006
 A;Accession: A60224
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <MD>
 C;Superfamily: proenkephalin
 C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGSF 5
 Db 1 YGGF 4

RESULT 14
 A41117 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
 C;Species: Naja naja oxiana (Asian cobra, Oxus cobra)
 C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
 C;Accession: A41117
 R;Kreikenkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991

A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
 A;Reference number: A41117; PMID:91296772; PMID:2068091

A;

Accession:

A41117

Status:

Preliminary

A;

Molecule type:

protein

A;

Residues:

1-8 <KRE>

A;

Cross-references:

UNIPROT:Q71Z27

C;

Keywords:

carboxylic ester hydrolase

Query Match 28.4%; Score 19; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

:|:|

7 SBLW 10

Db

2 AEMW 5

RESULT 15

A60410
beta-neoendorphin / dynorphin precursor - guinea pig precursor

N;Alternate names: alpha-neoendorphin; proenkephalin B precursor

C;Species: Cavia porcellus (guinea pig)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000

C;Accession: A60410

R;Murphy, R.; Turner, C.A.

Peptides 11, 65-68, 1990

A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.

A;Reference number: A60410; PMID:90259864; PMID:2342991

A;Accession: A60410

A;Molecule type: protein

A;Residues: 1-10 <MGR>

C;Superfamily: proenkephalin

C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

2 YGSF 5

| |

1 YGGF 4

Search completed: April 27, 2005, 15:43:23
 Job time : 45 secs

RA Figueiro F.; Sultmann H.; Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT class II loci";
 RL Genetics 149:1527-1537(1998).
 DR EMBL: AF050006; AAC1345..1.; -.
 FT NON-TER 1 1
 FT NON-TER 11 11
 SEQ SEQUENCE 11 AA; 1399 MW;
 SQ 3F47DB7A772685A3 CRC64;

Query Match Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0;

Qy 5 FFSELW 10
 Db 3 FWMLW 8

RESULT 3
 P83537 PRELIMINARY; PRT; 11 AA.
 ID P83537; AC P83537;
 DR 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 OS Homo sapiens (Human).
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lulli L.; Torchiana B.; Pinocchiaro G./
 RL Submitted (NOV-1996) to the ENBML/GenBank/DDJBJ databases.
 DR EMBL; U77631; AAD15626..1.; -
 DR GO:0004336; P:Galactosylceramidase activity; IEA.
 DR GO:0016798; P:Hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON-TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADD2C99C8 CRC64;

CC - INDUCTION: By elevated hydrostatic pressure.
 CC - INDUCTION: On the 2D-gel the determined MW of this unknown
 CC protein is: 65 kDa.
 FT NON-TER 1 1
 FT NON-TER 11 11
 SEQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0;

Qy 3 GSFFFS 7
 Db 1 GSFFFA 5

RESULT 4
 Q9TRT7 PRELIMINARY; PRT; 12 AA.

AC Q9TRT7; Q9TRT7; AC Q9TRT7;
 DR 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 15 kDa amyloid protein A homolog (Fragment).
 OS Bos taurus (Bovine).
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 Bovine; Bos
 OC Sequences; Bos
 RN [1]
 RP Veiby O.P.; Sletten K.; Husby G.; Nordstoga K.;
 RA "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 RT

RT of bovine kidney."; 35:63-69(1992).
 RL Scand. J. Immunol. 1 1
 FT NON-TER 1 1
 FT NON-TER 12 12
 SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AEB CRC64;

Query Match Score 22; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 6.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

Qy 4 SFFSELW 10
 Db 1 SFFXEXY 7

RESULT 5
 Q95953 PRELIMINARY; PRT; 9 AA.

ID Q95953; AC Q95953;
 DR 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DR Galactocerobrosidase (EC 3.2.1.46) (Fragment).
 GN Name=GALC;
 OS Homo sapiens (Human).
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RA Lulli L.; Torchiana B.; Pinocchiaro G./
 RL Submitted (NOV-1996) to the ENBML/GenBank/DDJBJ databases.
 DR EMBL; U77631; AAD15626..1.; -
 DR GO:0004336; P:Galactosylceramidase activity; IEA.
 DR GO:0016798; P:Hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON-TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADD2C99C8 CRC64;

CC - INDUCTION: By elevated hydrostatic pressure.
 CC - INDUCTION: On the 2D-gel the determined MW of this unknown
 CC protein is: 65 kDa.

FT NON-TER 1 1
 FT NON-TER 11 11
 SEQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0;

Qy 3 GSFFFS 7
 Db 1 GSFFFA 5

RESULT 6
 Q6LA62 PRELIMINARY; PRT; 10 AA.

ID Q6LA62; AC Q6LA62;
 DR 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Amiloride-sensitive epithelial sodium channel gamma subunit
 DE (Fragment).
 GN Name=SCNN1G;
 OS Homo sapiens (Human).
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96121599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
 RA Thomas C.P.; Doggett N.A.; Fisher R.; Stokes J.B.;
 RT "Genomic organization and the 5' flanking region of the gamma subunit
 of the human amiloride-sensitive epithelial sodium channel.";
 RL J. Biol. Chem. 271:26062-26066(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RA "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 RT

RESULT 7
 MEDLINE#98316780; PubMed=9654208;
 RA Ludwig M., Bolkenius U., Wickert L., Marynen P., Bidlingmaier F.;
 RT "structural organization of the gene encoding the alpha-subunit of the
 human amiloride sensitive epithelial sodium channel.";
 RL Hum. Genet. 102:576-581(1998).
 EMBL; CABN#7506.1; -;
 DR GO: GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 PT NON-TER 1 1
 FT NON-TER 10 10
 SQ SEQUENCE 10 AA; 1157 MW; DBAFF813373B05A2 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 SFPSFLW 10
 Db 1 SVVSEKWN 7

RESULT 7
 ID P92576 PRELIMINARY; PRT; 10 AA.
 AC P92576;
 DT 01-MAY-1997 (TRIMBLrel. 03; Created)
 DT 01-MAY-1997 (TRIMBLrel. 03; Last sequence update)
 DT 01-OCT-2003 (TRIMBLrel. 25; Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COL;
 OS Bipos biporus (Baja worm lizard).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
 OC NCBITAXID=52188; [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE#97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-itrand replication in
 rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE#97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replicon slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39 (1997).
 EMBL; U71355; AAB48271.1; -;
 PIR; T13838; T13838.
 KW Mitochondrion.
 PT NON-TER 10 10
 SQ SEQUENCE 10 AA; 1176 MW; SB3580C9D5A411A7 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFPS 7
 Db 6 SFPS 9

RESULT 8
 CORZ PERAM STANDARD; PRT; 11 AA.
 AC P114956; [1]
 DT 01-OCT-1989 (Rel. 12; Created)
 DT 01-FEB-1994 (Rel. 28; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Corazonin.

OS Periplaneta americana (American cockroach).
 OC Bkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea.
 OC Blattidae; Periplaneta.
 OX NCBI_TAXID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cordova cardíaca;
 RX MEDLINE#89325572; PubMed=27533132; DOI=10.1016/0014-5793(89)80727-6;
 RA Veensra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach."
 RL FEBS Lett. 250:231-234 (1989).
 CC -1- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Amidation; Direct protein sequencing; Neuropeptide;
 KW Pyrrolidone carboxylic acid.
 PT MOD-RES 1 1 Pyrrolidone carboxylic acid.
 PT MOD-RES 11 11 Asparagine amide.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFE32D6415AB46 CRC64;
 Query Match 29.9%; Score 20; DB 1; Length 11;
 Best Local Similarity 42.3%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 FSELWTS 12
 Db 5 YSRGWTN 11

RESULT 9
 ID 077894 PRELIMINARY; PRT; 11 AA.
 AC 077894; [1]
 DT 077894; Created
 DT 01-NOV-1998 (TRIMBLrel. 08; Last sequence update)
 DT 01-NOV-1998 (TRIMBLrel. 19; Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia).
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 RN NCBITAXID=8128; [1]
 RP SEQUENCE FROM N.A.;
 RX MEDLINE#98315113; PubMed=9649539;
 RA Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincent K.V.,
 RA Figuerola P., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 Genetics 149:1527-1537 (1998).
 RL EMBL; AF050004; AAC41343.1; -.
 DR NON-TER 1 1
 PT NON-TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
 Query Match 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 FFSELW 10
 Db 3 FWSIVW 8

RESULT 10
 ID 077898 PRELIMINARY; PRT; 11 AA.
 AC 077898; [1];
 DT 077898; [1];
 OX NCBITAXID=6978; [1];
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cordova cardíaca;
 RX MEDLINE#89325572; PubMed=27533132; DOI=10.1016/0014-5793(89)80727-6;
 RA Veensra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach."
 RL FEBS Lett. 250:231-234 (1989).
 CC -1- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Amidation; Direct protein sequencing; Neuropeptide;
 KW Pyrrolidone carboxylic acid.
 PT MOD-RES 1 1 Pyrrolidone carboxylic acid.
 PT MOD-RES 11 11 Asparagine amide.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFE32D6415AB46 CRC64;

01-NOV-1998 (TrEMBLref. 08; Last sequence update)
 DT DT -DBC-2001 (TrEMBLref. 19; Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Buteostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidei;
 Cichlidae; Oreoichromis.
 NCBI_TAXID=8128;
 RN
 RP SEQUENCE FROM N.A.; PubMed=9649539;
 RX MEDLINE=98131511A;
 RA Malaga-Trillo B.; Zaleska-Rutczynska Z.; McAndrew B.; Vincsek V.;
 RA Figueras F.; Sulmann H.; Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci.";
 RU Genetics 148:1527-1537(1999).
 DR EMBL; AF050008; AAC41347.1; -.
 FT NON-TER 1 1
 SQ SEQUENCE 11 AA.; 1136 MW.; 3F47DC0A62C045A3 CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 RESULT 11
 Qy 5 PFPSEIW 10
 Db 3 FWSIVW 8
 SQ SEQUENCE FROM N.A.;
 ID Q65CG7 PRELIMINARY; PRT; 11 AA.
 AC Q65CG7;
 DT 25-OCT-2004 (TrEMBLref. 28; Created)
 DT 25-OCT-2004 (TrEMBLref. 28; Last sequence update)
 DT 25-OCT-2004 (TrEMBLref. 28; Last annotation update)
 DE Transcriptional activator (Fragment).
 GN Name=AC22;
 OS Tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TAXID=71186;
 RN RP SEQUENCE FROM N.A.;
 RC STRAINNI3;
 RA Rojas A.; Kvarnheiden A.; Rodriguez D.; Valkonen J.P.T.;
 RT "A mixture of begomoviruses in severe, leaf curl-affected tomatoes in
 Nicaragua.";
 RT Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ508781; CAD48523.1; -.
 FT NON-TER 1 1
 SQ SEQUENCE 11 AA.; 1356 MW.; 861BC90602D379DS CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 SPPSELMNT 11
 Db 4 SFWVELFES 11
 SQ SEQUENCE FROM N.A.;
 ID Q46664 PRELIMINARY; PRT; 12 AA.
 AC Q46664;
 DT 01-JUN-1998 (TrEMBLref. 06; Created)
 DT 01-JUN-1998 (TrEMBLref. 06; Last sequence update)
 DT 01-JUN-1998 (TrEMBLref. 06; Last annotation update)
 DE Glucose-6-phosphate dehydrogenase (Fragment).
 GN Name=G6PD;
 OS Macropus robustus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 NCBI_TAXID=35589;
 RN [1]
 RP SEQUENCE FROM N.A.;
 RX MEDLINE=9724585; PubMed=9060417;
 RA Loebel D.A.; Johnston P.G.;
 RT "Analysis of the intron-exon structure of the G6PD gene of the
 wallaroo (Macropus robustus) by polymerase chain reaction."
 RL Mamm. Genome 8:146-147(1997).
 DR EMBL; U533774; AAC48789.1; -.
 FT NON-TER 1 1
 SQ SEQUENCE 12 AA.; 1430 MW.; D42A9C84E3CB1AA9 CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 GSFFESSE 8
 Db 2 GYFDFD 7
 RESULT 13
 Q61331 PRELIMINARY; PRT; 12 AA.
 ID Q61331; PRT; 12 AA.
 AC Q61331;
 DT 01-NOV-1996 (TrEMBLref. 01; Created)
 DT 01-MAY-1999 (TrEMBLref. 10; Last sequence update)
 DT 01-JUN-2003 (TrEMBLref. 24; Last annotation update)
 DS N-acetylglucosamine beta1-4 galactosyl transferase (EC 2.4.1.90)
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10509;
 RN
 RP SEQUENCE FROM N.A.;
 RX MEDLINE=89033997; PubMed=3141392;
 RA Nakazawa K.; Ando T.; Kimura T.; Marimatsu H.;
 RT "Cloning and sequencing of a full-length cDNA of mouse N-
 acetylglucosamine (bet-1-4)galactosyl transferase.";
 RT acetylglucosamine (bet-1-4)galactosyl transferase.
 RL J. Biochem. 104:165-168(1988).
 DR EMBL; D00315; BAA00217.1; -.
 DR GO; GO:0003945; P:N-acetyl-lactosamine synthase activity; IEA.
 DR GO; GO:0016757; P:transferase activity, transferring glycosyl; IEA.
 KW Glycosyltransferase; Transferase.
 FT NON-TER 1 1
 SQ SEQUENCE 12 AA.; 1283 MW.; 304EA40668387728 CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 WTS 12
 Db 1 WTS 3
 RESULT 14
 FARP_MONEY STANDARD; PRT; 6 AA.
 ID FARP_MONEY
 AC P41966;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DS FMRFamide-like neuropeptide GNFRP-amide.
 OS Monodelphis expansa (Sheep tapeworm)
 OC Eukaryota; Metazoa; Playyhelminthes; Cestoda; Eucestoda;
 OC Cyclopolyidae; Anoplocephalidae; Moniezia.
 NCBI_TAXID=28841;

```

RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G.; Shaw C.; Halton D.W.; Thim L.;  

RT "GNFFRamide: a novel FMRFamide immunoreactive peptide isolated from  

the sheep tapeworm, Moniezia expansa.";  

RL Biochim. Biophys. Res. Commun. 193:1054-1060(1993).
CC -1-
CC SUBCELLULAR LOCATION: Secreted.
CC -1-
CC SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC PIR: A43129; A43129.
KW Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 6
FT Phenylalanine amide.
SEQUENCE 6 AA; 787 MW; 69D409C9c481000 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 3 GSFP 6
:|:
Db 1 GNFF 4

RESULT 15
Q99MNO
ID Q99MNO PRELIMINARY; PRT; 8 AA.
AC Q99MNO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
GN Name=adat1;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=129/SvJ;
RX MEDLINE=21231131; PubMed=11331948;
RA Maas S.; Kim Y.-G.; Rich A. ;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two  

tRNA synthetases.";
RL Mamm. Genome 12:387-393 (2001).
DR EMBL; AF32904; AK19310.1; -
DR MGD; MGI:1353363; Addt:1.
PT NON-TER 8 8
SEQUENCE 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;

Query Match 28.4%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 9 IWTs 12
:|:
Db 1 MWTs 4

Search completed: April 27, 2005, 15:46:23
Job time : 176 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:39:49 ; Search time 167 Seconds (without alignments)

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:
 1: geneseqp1980B:
 2: geneseqp1980B:
 3: geneseqp2000B:
 4: geneseqp2001B:
 5: geneseqp2002B:
 6: geneseqp2003Ab:
 7: geneseqp2003Bs:
 8: geneseqp2004B:
 8: geneseqp2004Bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	82.1	12	4 AAB86005	Aab86005 DCM-associat
2	34	50.7	6	5 AAM47222	Aab97294 Beta1-adr
3	34	50.7	6	5 ADP49242	Aam47222 Dilated c
4	34	50.7	6	3 AAB09130	Adp49242 Disease-a
5	34	50.7	8	3 AAB09130	Aab97294 Hepatitis
6	31	46.3	10	8 ADK09671	Aab97294 Human pap
7	31	46.3	10	8 ADK09188	Adk09671 Human pap
8	30	44.8	6	5 ABR46515	Abr46515 Staphyloc
9	30	44.8	9	2 AAW72493	Aaw72493 Dengue vi
10	30	44.8	10	2 AAW76040	Aaw76040 LM609 Gra
11	30	44.8	10	2 AAW37198	Aaw37198 Human onc
12	30	44.8	10	4 AAB61398	Aab61398 Multiple
13	30	44.8	10	6 ABO19836	Abo19836 Enhanced
14	30	44.8	10	7 ADG71874	Enhanced Adg71874
15	30	44.8	10	8 ADG51055	Adg71874 Enhanced
16	29	43.3	7	2 AAY33139	Adg51055 Murine LM
17	29	43.3	10	5 AAU93215	Aay33139 Rabbit ca
18	29	43.3	11	6 ABJ37125	Aau93215 Granulocy
19	29	43.3	12	4 AAM00568	Abj37125 Rhodopain
20	28	41.8	6	6 ABR46459	Aam00568 Human str
21	28	41.8	7	8 ADR68302	Abr46459 Staphyloc
22	28	41.8	8	8 ADK09492	Adr68302 Androgen
23	28	41.8	9	8 AAY04678	Adk09492 Human pap
24	28	41.8	9	8 ADK09532	Aay04678 Peptide #
25	28	41.8	9	8 ADK09531	Adk09532 Human pap
					Adk09531 Human pap

ALIGNMENTS

RESULT 1									
AAB86005 standard; peptide: 12 AA.									
ID	AAB86005	XX	XX	XX	XX	XX	XX	XX	XX
AC	AAB86005;	AC	AC	AC	AC	AC	AC	AC	AC
DT	12-JUL-2001	(first entry)							
XX									
DB	DCM-associated peptide #5.	XX	XX	XX	XX	XX	XX	XX	XX
OS	Synthetic.	XX	XX	XX	XX	XX	XX	XX	XX
PN	WO200121660-A1.	PN	PN	PN	PN	PN	PN	PN	PN
XX									
PD	29-MAR-2001.	XX	XX	XX	XX	XX	XX	XX	XX
XX									
PP	21-SEP-2000; 2000WO-EPO09241.	XX	XX	XX	XX	XX	XX	XX	XX
PR	21-SEP-1999; 99EP-00118630.	PR	PR	PR	PR	PR	PR	PR	PR
XX									
PA	99EP-00118631.	XX	XX	XX	XX	XX	XX	XX	XX
(AFPI-)	APPINA IMMUNOTECHNIK GMBH.								
XX									
PI	Roenspeck W, Kunze R, Wallukat G, Dierenthal M;	XX	XX	XX	XX	XX	XX	XX	XX
XX									
DR	WPI; 2001-335469/35.	XX	XX	XX	XX	XX	XX	XX	XX
XX									
PT	New peptide useful for combating the autoantibodies that are responsible for dilative cardiomyopathy.	XX	XX	XX	XX	XX	XX	XX	XX
PT									
PS	Claim 3: Page 20: 29pp; German.	XX	XX	XX	XX	XX	XX	XX	XX
XX									
CC	This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiac and immunosuppressive activity.	CC	CC	CC	CC	CC	CC	CC	CC
CC	used to produce medicine to combat beta 1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention	CC	CC	CC	CC	CC	CC	CC	CC
XX									
SQ	Sequence 12 AA;	XX	XX	XX	XX	XX	XX	XX	XX
Query Match	82.1%	Score 55;	DB 4;	Length 12;					
Best Local Similarity	100.0%	Pred. No.	0.013;						

XX AC ADP49242; XX OS Hepatitis GB virus.
 XX DT 09-SEP-2004 (First entry) XX PN US6051374-A.
 XX Disease-associated autoantibody detection method peptide #1. XX
 XX KW cardiant; synaecological; immunosuppressive; hypotensive; antipsoriatric;
 XX G protein-coupled receptor. XX
 XX Unidentified. XX
 OS WO2004051280-A2. XX
 PN PR 07-JUN-1995; 95US-00488445.
 XX PD 17-JUN-2004. XX
 XX (ABBOT LAB. PA
 XX PF 28-NOV-2003; 2003WO-DE003988. XX
 XX PR 29-NOV-2002; 2002DE-01056897. PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
 XX PR 27-JAN-2003; 2003DE-01003120. PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 PR 13-JUN-2003; 2003DE-01027066. XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX. DR WPI; 2000-338307/29.
 PI Wallukat G; XX
 DR WPI; 2004-450802/42. XX
 XX Detecting disease-associated autoantibodies against G protein-coupled
 PT receptors, useful for diagnosing e.g. cardiomyopathy, comprises an
 PT enzymatic or color reaction. XX
 PS Claim 12; Page 49; 57PP; German.
 XX The present invention relates to a method for detecting disease-
 CC associated autoantibodies (AAb) directed against G protein-coupled
 CC receptors. This comprises treating a body fluid with a denaturing agent,
 CC treating the precipitate formed with a biotin-containing peptide having
 the (partial) sequence of a first and/or second loop of a G protein-
 CC coupled receptor, incubating the mixture with a carrier coated by
 CC (script) avidin, washing the carrier and incubating it with labeled anti-
 CC immunoglobulin G (IgG) antibody subclasses, and performing an enzymatic
 CC or colour reaction. The method is used to detect AAb associated with
 CC dilatative or Chagas cardiomyopathy, myocarditis, pre-eclampsia, humoral
 CC kidney rejection, malignant, essential, refractory or pulmonary
 CC hypertension, psoriasis and Raynaud's syndrome. The present invention is
 CC a peptide which can be used in the method of the invention.
 XX
 SQ Sequence 6 AA:
 Query Match 50.7%; Score 34; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
 SQ 1 EYGSFF 6
 1 |||||
 Db 1 EYGSFF 6
 SQ RESULT 5
 AAB09130 ID AAB09130 standard; protein; 8 AA.
 XX AC AAB09130;
 XX DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (First entry)
 XX DB Hepatitis GB virus sequence SEQ ID NO:252.
 XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis.

XX OS Hepatitis GB virus.
 XX PN US6051374-A.
 XX PD 18-APR-2000.
 XX PR 07-JUN-1995;
 XX PR 07-JUN-1995; 95US-00488445.
 PR 14-FEB-1994; 94US-00196030.
 PR 13-MAY-1994; 94US-0024654.
 PR 29-JUL-1994; 94US-01028314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-0037557.
 XX PA (ABBOT LAB.
 XX PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
 XX PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX XX DR WPI; 2000-338307/29.
 XX Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the HGBV
 PT polynucleotide probe and detecting the complex that contains target HGBV.
 XX PS Example 9; Col 331-332; 369pp; English.
 XX The present invention describe a method for detecting target hepatitis GB
 CC virus (HGBV) nucleic acid (Tm) in a test sample (T) with suspected of
 CC containing HGBV. The method involves reacting (T) with a HGBV
 CC polynucleotide probe (P) containing 15 contiguous nucleotides, and which
 CC selectively hybridizes to the HGBV genome or its full complement, and
 CC detecting the complex that contains Tm, indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -B hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AA55489 and AAB0985 to AAB09480 represent nucleotide and
 CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS Field.)
 XX SQ Sequence 8 AA:
 Query Match 50.7%; Score 34; DB 3; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Delins 0; Gaps 0;
 SQ 6 FSEELWTS 12
 6 |||||
 Db 1 FSHLWTS 7
 SQ RESULT 6
 AAB09671 ID AAB09671 standard; peptide; 10 AA.
 XX AC AAB09671;
 XX XX DR 06-MAY-2004 (First entry)
 DB Human papillomavirus peptide #1726.
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW viricide; vaccine; therapeutic agent; infection; HPV.
 XX OS Human papillomavirus.
 XX PN WO2004011650-A2.
 XX PD 05-FEB-2004.

CC	inflammation reactions.	The diseases or disorders include cardiovascular
CC	diseases, disease of the central nervous system, gastrointestinal	
CC	diseases, skin diseases, genitourinary diseases, joint diseases,	
CC	respiratory diseases and HIV infection	
SQ	Sequence 6 AA:	
Qy	Query Match 44.8%; Score 30; DB 6; Length 6;	
Best Local Similarity 83.3%; Pred. No. 1.8e+06;		
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Db	5 FFSELW 10 1 FFPFLW 6	
RESULT 9		
ID AAW72493		
AAW72493 standard; peptide, 9 AA.		
XX		
AC AAW72493;		
XX		
DT 23-DEC-1998	(first entry)	
XX		
DS Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #38.		
XX		
KW Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;		
KW dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;		
KW immunisation; immunoreactive; infection.		
XX		
OS Dengue virus.		
XX		
US5824506-A.		
XX		
PD 20-OCT-1998.		
XX		
PP 15-AUG-1994;	94US-00290268.	
XX		
PR 15-AUG-1994;	94US-00290268.	
XX		
PA (GENE-) GENELABS DIAGNOSTICS PTE LTD.		
XX		
PI Chan L, Guan M;		
XX		
DR WPI: 1998-582552/49.		
XX		
PT Dengue virus peptide antigens - especially for diagnosis of dengue virus		
PT infection.		
XX		
PS Example 1; Col 17; 21pp; English.		
XX		
CC AAW72570 represent Peptide fragments from the dengue virus		
CC type-2 glycoprotein NS1, which was used in an example from the present		
CC invention for an epitope mapping assay. The invention has developed		
CC peptide antigens consisting of fragments of the dengue virus NS1 protein.		
CC The peptide antigens can be used for the diagnosis of dengue virus		
CC infection by detection of antibodies to the virus, especially in an assay		
CC comprising attaching the antigen to a solid support, contacting a serum		
CC sample with the support, and detecting bound antibodies with a labelled		
CC anti-human antibody or used for preparing vaccines against dengue virus		
CC infection		
XX		
SQ Sequence 9 AA:		
Qy Query Match 44.8%; Score 30; DB 2; Length 9;		
Best Local Similarity 50.0%; Pred. No. 1.8e+06;		
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;		
Db 3 GSFFSELW 10 1 GVPFTNW 8		

DE Human oncogenic protein MDM2 binding Cys (Acrlid) peptide derivative 2.
 XX
 KW MDM2; Oncogenic protein; p53; human; inhibition; interaction; cancer;
 tumour; diagnosis; binding; viral infection.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 Modified-site 1 /note= "N-terminal acetyl; Sulphydryl side-chain linked
 to 6-acryloyl-2-(dimethylamino)naphthalene"
 FT
 Modified-site 10 /note= "C-terminal amide"
 XX
 WO9801467-A2.
 PN
 XX
 PD 15-JAN-1998.
 PP 04-JUL-1997; 97WO-EP003549.
 PR 05-JUL-1996; 96GB-00014197.
 PR 07-APR-1997; 97GB-00007041.
 PA (NOVS) NOVARTIS AG.
 PB (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Lane D, Boettger V, Boettger A, Picklesay S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 XX
 DR 1998-100996/09.
 PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 XX
 Example 2; Page 20; 45pp; English.
 PS This is a Cys (Acrlid) peptide derivative capable of binding to a human
 oncogenic protein MDM2. The MDM2 binding peptides can specifically
 inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 induce growth arrest or apoptosis in tumour cells comprising a wild-type
 p53 and non-elevated levels of MDM2. The peptides may be used to identify
 molecules that bind to MDM2 and to identify and design inhibitors of
 MDM2/p53 binding. They may also be used to purify binding partners
 especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 cancer and leukaemia patients and for treatment or prevention of disease
 involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 injection. By interfering with MDM2/p53 interaction, the peptides can
 activate p53 function and accumulation in normal cells. The peptides
 which mimic the MDM2 binding site in p53, have a significantly greater
 blocking activity compared with wild-type p53
 XX
 Sequence 10 AA:
 SQ Query Match 44.8%; Score 30; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 YY 2 YGSFPS 7
 DB 5 YGSFYS 10
 RESULT 13
 ABO19836 standard; peptide; 10 AA.
 XX
 AC ABO19836;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 Enhanced LM609 heavy chain variable region CDR3 #15.
 XX
 KW LM609; antibody; grafted antibody; alpha_vbeta_3; angiogenesis; CDR;
 KW alpha_vbeta_3-mediated disease; complementarity determining region;
 KW restenosis.
 XX
 OS Unidentified.
 XX
 PN US2003028009-A1.
 XX
 PD 06-FEB-2003.
 XX
 PP 06-JUL-2001; 2001US-0900590.
 XX
 DT
 RESULT 12
 AAB61398 standard; peptide; 10 AA.
 ID AAB61398
 XX
 AC AAB61398;
 XX
 DT 03-APR-2001 (first entry)

PR 30-JAN-1998; 98US-00016061.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 Huse WD;
 PI
 PT WPI; 2003-492042/46.
 XX
 DR N-PSDB; ACD30195
 XX
 PT New Vitaxin or LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3 useful for treating an alphavbeta3-mediated disease e.g., angiogenesis or restenosis.
 XX
 PS Clam 62; Page 13; 71pp; English.
 XX
 CC The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting selective binding affinity to alpha_vbeta_3. The Vitaxin or LM609 grafted antibody is useful for treating an alpha_vbeta_3-mediated disease e.g., angiogenesis or restenosis. The present sequence represents the amino acid sequence of a LM609 complementarity determining region
 XX Sequence 10 AA;
 SQ Query Match Score 44.8%; DB 6; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;
 DB 2 YGSFFS 7
 ||||:
 5 YGSFYS 10

RESULT 14
 ADG71874
 ID ADG71874 standard; protein; 10 AA.
 XX
 AC ADG71874;
 XX
 DT 11-MAR-2004 (first entry)
 DE Enhanced LM609 grafted antibody VH region CDR3 #15.
 XX
 KW Grafted antibody; high affinity; alphavbeta3; inflammatory disorder; complementarity determining region; CDR; inflammation; immune inflammation; non-immune inflammation;
 KW chronic articular rheumatism; psoriasis; vessel disorder;
 KW diabetic retinopathy; neovascular glaucoma; capillary proliferation;
 KW atherosclerotic plaque; cancer disorder; antiinflammatory; antirheumatic;
 KW dermatological; immunosuppressive; ophthalmological; humanised;
 OS Synthetic.
 OS Homo_sapiens.
 XX US6596850-B1.
 PN
 PD 22-JUL-2003.
 XX
 PP 30-JAN-1998; 98US-00016061.
 XX
 PR 30-JAN-1998; 98US-00016061.
 PA (IXSY-) IXSYS INC.
 XX
 PI Huse WD;
 XX
 DR WPI; 2003-842325/78.
 DR N-PSDB; A0871873.
 XX
 PT New high affinity LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3, useful for treating an alphavbeta3-mediated disease, e.g., angiogenesis and restenosis. The present sequence is murine LM609
 PT antibody variable region CDR mutant peptide.
 XX
 PS Claim 6; SEQ ID NO 100; 66pp; English.

XX
 CC The present invention relates to a high affinity LM609 grafted antibody exhibiting selective binding to alphavbeta3, or its functional fragment comprising one or more complementarity determining regions (CDRs) having at least one amino acid substitution in one or more CDRs of the LM609 grafted heavy chain variable region of a polypeptide having 117 amino acids or a grafted light chain variable region polypeptide having 107 amino acids. Also disclosed are polynucleotide sequences encoding the novel antibody or its functional fragment, and a composition comprising the novel antibody or its functional fragment. The antibodies and their fragments are useful for treating alphavbeta1-mediated diseases, e.g. inflammatory disorders such as immune and non-immune inflammation, chronic articular rheumatism, psoriasis, disorders associated with inappropriate or inopportune invasion of vessels such as diabetic retinopathy, neovascular glaucoma, and capillary proliferation in atherosclerotic plaques as well as cancer disorders. The present sequence represents an antibody region.
 XX
 SQ Sequence 10 AA;
 SQ Query Match Score 44.8%; DB 7; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;
 DB 2 YGSFFS 7
 ||||:
 5 YGSFYS 10

RESULT 15
 ADJ58055
 ID ADJ58055 standard; peptide; 10 AA.
 XX
 AC ADJ58055;
 XX
 DT 06-MAY-2004 (first entry)
 DE Murine LM609 heavy chain variable region (VH) CDR3 mutant peptide #15.
 XX
 KW Vitaxin; antibody; LM609; angiogenesis; restenosis; therapy;
 KW variable region; mouse; mutant; mitein.
 XX
 OS Synthetic.
 XX
 PN US2004006213-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 16-JUN-2003; 2003US-00463847.
 XX
 PI Huse WD, Glaser SM;
 XX
 DR WPI; 2004-081749/08.
 XX
 PT New Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3, useful for treating alphavbeta3-mediated diseases, e.g. angiogenesis or restenosis.
 XX
 PS Claim 62; SEQ ID NO 100; 69pp; English.

XX
 CC The present invention provides a Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alpha-v-beta-3. The invention is useful for treating alpha-v-beta-3-mediated diseases such as angiogenesis and restenosis. The present sequence is murine LM609
 CC antibody variable region CDR mutant peptide.
 XX
 SQ Sequence 10 AA;

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Query Match      44.8%; Score 30; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. Nc. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;

Qy          2 YGSFFS 7
Db          5 YGSYS 1.0
```

Search completed: April 27, 2005, 15:49:16
Job time : 169 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:40:23 ; Search time 41 Seconds (without alignments)

21.849 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 BYGSEFFSELWTS 12

Scoring table: BL03M62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cggn2_6/prodata/1/iaa/5A_COMB_pep:*

2: /cggn2_6/prodata/1/iaa/5B_COMB_pep:*

3: /cggn2_6/prodata/1/iaa/6A_COMB_pep:*

4: /cggn2_6/prodata/1/iaa/6B_COMB_pep:*

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6: /cggn2_6/prodata/1/iaa/backfiles_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-10-088-681-2

; Sequence 252, Application US/08469260A

; Patent No. 6451578

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DEBAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOF
; APPLICANT: JAMES C. ERICK
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469_260A
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/424_550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; ALIGNMENTS

; Sequence 19, App1

; Sequence 15, App1

; Sequence 19, App1

; Sequence 7, App1

; Sequence 11, App1

; Sequence 18, App1

; Sequence 11, App1

; Sequence 18, App1

; Sequence 18, App1

; Sequence 19, App1

; Sequence 10, App1

; Sequence 11, App1

; Sequence 11, App1

; Sequence 12, App1

; Sequence 13, App1

; Sequence 11, App1

; Sequence 19, App1

; Sequence 10, App1

; Sequence 11, App1

; Sequence 12, App1

; Sequence 13, App1

; Sequence 14, App1

; Sequence 15, App1

; Sequence 16, App1

; Sequence 17, App1

; Sequence 18, App1

; Sequence 19, App1

; Sequence 20, App1

; Sequence 21, App1

; Sequence 22, App1

; Sequence 23, App1

; Sequence 24, App1

Result No.	Score	Query Match	Length	DB ID	Description
1	34	50.7	8	4 US-08-669-260A-252	Sequence 252, App1
2	34	50.7	8	4 US-08-488-446-252	Sequence 252, App1
3	34	50.7	8	4 US-08-467-344A-252	Sequence 252, App1
4	34	50.7	8	4 US-08-424-550B-252	Sequence 252, App1
5	30	44.8	6	1 US-08-424-957/-6	Sequence 6, App1
6	30	44.8	6	3 US-09-035-686-6	Sequence 6, App1
7	30	44.8	10	4 US-09-339-922A-100	Sequence 100, App1
8	30	44.8	10	4 US-09-016-061-100	Sequence 100, App1
9	30	44.8	11	3 US-08-424-957-42	Sequence 42, App1
10	30	44.8	11	3 US-09-035-686-42	Sequence 42, App1
11	29	43.3	7	4 US-09-535-686B-10	Sequence 10, App1
12	29	43.3	10	4 US-09-520-091-28	Sequence 28, App1
13	28	41.8	11	3 US-09-186-958-6	Sequence 6, App1
14	28	41.8	11	3 US-09-659-211A-6	Sequence 6, App1
15	28	41.8	11	4 US-09-381-216-6	Sequence 6, App1
16	27.5	41.0	9	1 US-08-931-635-50	Sequence 50, App1
17	27.5	41.0	9	3 US-09-535-686B-10	Sequence 50, App1
18	27.5	41.0	9	5 PCT-US94-01258-50	Sequence 50, App1
19	27.5	41.0	9	5 PCT-US95-11235-50	Sequence 50, App1
20	27	40.3	6	1 US-08-277-660A-2	Sequence 2, App1
21	27	40.3	6	1 US-08-424-957-2	Sequence 2, App1
22	27	40.3	6	3 US-09-300-386A-50	Sequence 2, App1
23	27	40.3	6	4 US-09-081-975-1	Sequence 1, App1
24	27	40.3	6	4 US-09-128-022B-130	Sequence 130, App1
25	27	40.3	6	4 US-09-332-384-4	Sequence 4, App1
26	27	40.3	7	1 US-08-277-660A-27	Sequence 27, App1
27	27	40.3	7	1 US-08-424-957-15	Sequence 15, App1

US-08-469-260A-252

Query Match 50.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELMNTS 12
 Db 1 FSHLWTS 7

RESULT 2

US-08-488-446-252

; Sequence 252, Application US/08488446

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; PATENT NO. 6536568

; GENERAL INFORMATION:

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES

; STREET: 100 ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467,344A

; FILING DATE: 07-Jun-1995

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/424,550

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 252:

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,550

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 252:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-488-446-252

RESULT 3

US-08-467-344A-252

; Sequence 252, Application US/08467344A

; PATENT NO. 6536568

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES

; STREET: 100 ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,446

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,550

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 252:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-467-344A-252

Query Match 50.7%; Score 34; DB 4; Length 8;

Best Local Similarity 85.7%; Pred. No. 4.1e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELMNTS 12

Db 1 FSHLWTS 7

RESULT 4

US-08-424-550B-252

; Sequence 252, Application US/08424550B

; PATENT NO. 6720156

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES

; STREET: 100 ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467,344B

; FILING DATE: 07-Jun-1995

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/424,550

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 252:

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,550

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 252:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-424-550B-252

Query Match 50.7%; Score 34; DB 4; Length 8;

Best Local Similarity 85.7%; Pred. No. 4.1e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELMNTS 12

Db 1 FSHLWTS 7

RESULT 3

৩

Query Match 44.8%; Score 30; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELW 10
 Db 2 FSELW 6

RESULT 7
 US-09-339-922A-100
 ; Sequence 100, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; ATTORNEY: WU, Herren
 ; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
 ; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; NUMBER OF SEQ ID NOS: 112
 ; SEQ ID NO: 100
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Mutated
 ; OTHER INFORMATION: complementarity determining region (CDR)
 ; US-09-339-922A-100

Query Match 44.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 83.3%; Pred. No. 66;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
 Db 5 YGSFFS 10

RESULT 8
 US-09-16-061-100
 ; Sequence 100, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; ATTORNEY: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; TELEPHONE: (415) 781-1989

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 STRANDEDNESS:
 TYPE: amino acid

US-08-424,957-42

Query Match 44.8%; Score 30; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELW 10
 Db 5 YGSFFS 10

Db 5 FSBLW 9

RESULT 10
US-09-035-686-42 Application US/09035686
Sequence 42, Application US/09035686
Patent No. 6153391
GENERAL INFORMATION:
APPLICANT: Pickley, Steven M.
ATTORNEY: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
ZIP: United States
94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,686
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1919
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
STRANDEDNESS:
TOPOLOGY: unknown
US-09-035-686-42

Query Match Score 29; DB 4; Length 10;
Best Local Similarity 44.8%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSBLW 10
Db 5 FSBLW 9

PRIOR FILING DATE: 1998-02-19
PRIORITY NUMBER: PCT/US99/03171
PRIORITY FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 7
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-595-682B-10

RESULT 11
US-09-595-682B-10 Application US/09595682B
Sequence 10, Application US/09595682B
Patent No. 6800483
GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tumor Cells
FILE REFERENCE: SU-005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258

Query Match Score 29; DB 4; Length 10;
Best Local Similarity 43.3%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFSELW 10
Db 1 AFWELW 7

PRIOR FILING DATE: 1998-02-19
PRIORITY NUMBER: PCT/US99/03171
PRIORITY FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 7
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-595-682B-10

RESULT 12
US-09-620-091-28 Application US/09620091
Sequence 28, Application US/09620091
Patent No. 6716811
GENERAL INFORMATION:
APPLICANT: CIRILA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: PIPLANI, SUNILALA
APPLICANT: MERRILL, BARBARA MCBOWEN
APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED TITLE OF INVENTION: USES OF INVENTION: USES
FILE REFERENCE: 03100-0014
CURRENT APPLICATION NUMBER: US/09/620,091
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-620-091-28

RESULT 13
US-09-186-958-6 Application US/09186958B
Sequence 6, Application US/09186958B
Patent No. 6238860
GENERAL INFORMATION:
APPLICANT: Whelinan, E. Fayette
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: Dyax-009-00 US Sequence listing
CURRENT APPLICATION NUMBER: US/09/186,958B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 US-09-186-958-6

Query Match 41.8%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 FFSEBLWTS 12
 Db 1 FFCALWPS 8

RESULT 14
 US-09-669-271A-6
 Sequence 6, Application US/09669271A
 Patent No. 6291197
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayette
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 FILE REFERENCE: Dyax 009.0 US sequence listing
 CURRENT APPLICATION NUMBER: US/09/669,271A
 CURRENT FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 US-09-669-271A-6

Query Match 41.8%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 FFSEBLWTS 12
 Db 1 FFCALWPS 8

RESULT 15
 US-09-881-276-6
 Sequence 6, Application US/09881276
 Patent No. 6479641
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayette
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 FILE REFERENCE: DIX-009.0 US 2
 CURRENT APPLICATION NUMBER: US/09/881,276
 CURRENT FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: 09/1669,271
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Microsoft Word 97
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
 US-09-881-276-6

Query Match 41.8%; Score 28; DB 4; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length	DB ID	Description
1	34	50.7	6	16 US-10-221-042-2	Sequence 2, Appli
2	34	50.7	8	US-08-424-550B-252	Sequence 252, App
3	30	44.8	10	9 US-09-214-371-35	Sequence 35, Appli
4	30	44.8	10	9 US-09-214-371-36	Sequence 36, Appli
5	30	44.8	10	10 US-09-900-590-100	Sequence 100, App
6	30	44.8	10	14 US-10-505-231-100	Sequence 100, App
7	30	44.8	10	15 US-10-463-847-100	Sequence 100, App
8	29	43.3	10	17 US-10-559-207-28	Sequence 28, Appli
9	28	41.8	9	US-09-486-73A-35	Sequence 35, Appli
10	28	41.8	11	9 US-09-881-276-6	Sequence 6, Appli
11	28	41.8	11	15 US-10-417-895A-56	Sequence 56, Appli
12	27	40.3	6	9 US-09-214-371-83	Sequence 83, Appli
13	27	40.3	6	9 US-09-732-384-4	Sequence 4, Appli

RESULT 2 US-08-424-550B-252
 Sequence 252, Application US/08424550B
 Publication No. US20020119447A1
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT NUERHOFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUIJK
 APPLICANT: ISA K. MUSHAWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550B
 FILING DATE: 4/35435
 CLASSIFICATION: 435435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMBSKI, PRISCILLA B.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-3623
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-424-550B-252

Query Match Score 34; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.3e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSBLWTS 12
 Db 1 FSHLWTS 7

RESULT 3 US-09-214-371-35
 Sequence 35, Application US/09214371B
 GENERAL INFORMATION:
 APPLICANT: Lane, David
 APPLICANT: Bottger, Volker
 APPLICANT: Bottger, Angelica
 APPLICANT: Picklesley, Stephen
 APPLICANT: Chene, Patrick
 APPLICANT: Hochkeppel, Heinz-Kurt
 APPLICANT: Garcia-Echeverria, Carlos
 APPLICANT: Furet, Pascal

Query Match Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFFSELW 10
 Db 2 GPTFSDLW 9

RESULT 5

US-09-900-590-100
Sequence 1.00, Application US/09900590
Publication No. US201003008009A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
NAME: Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 1.00

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-3001
TELEFAX: (619) 535-8919

INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-900-590-100

Query Match 44.8%; Score 30; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
Db 5 YGSFYS 10

RESULT 6

US-10-305-331-100
Sequence 1.00, Application US/10305231
Publication No. US201003166872A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herran

TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use

FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/10/305,231
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/09/339,922
PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100

Query Match 44.8%; Score 30; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
Db 5 YGSFYS 10

RESULT 8
US-10-659-207-28
Sequence 28; Application US/10659207
Publication No. US20050037959A1
GENERAL INFORMATION:
APPLICANT: CWIRLA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: MERRILL, BARBARA MCEOWEN
APPLICANT: PIRIANT, SUNILIA
APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED TITLE OF INVENTION: USES FILE REFERENCE: 03/00-0014
CURRENT APPLICATION NUMBER: US/10/659,207
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: US/09/620,091
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-659-207-28

Query Match Score 29; DB 17; Length 10;
Best Local Similarity 71.4%; Pred. No. 3.e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY | : |||
DB 3 SFVWELW 9

RESULT 9
US-09-486-734A-35
Sequence 35; Application US/09486734A
PATENT NO. US20020164732A1
GENERAL INFORMATION:
APPLICANT: Chopin, Marie-Christine
APPLICANT: Chier, Florence
APPLICANT: Erlich, S. Dusko
APPLICANT: Gautier, Michel
APPLICANT: Schouler, Catherine
TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
FILE REFERENCE: 33/339/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
PRIOR APPLICATION NUMBER: PC/T/FR98/01873
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hsds subunit
US-09-486-734A-35

Query Match Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41.8%; Score 28; DB 9; Length 9;
DB 1 SYSSWSS 9

RESULT 10
US-09-881-276-6
Sequence 6; Application US/09881276
PATENT NO. US20120031761A1
GENERAL INFORMATION:
APPLICANT: Whelihan, E. Fayelle
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: DXY-009; US-2
CURRENT APPLICATION NUMBER: US/09/881,276
CURRENT FILING DATE: 2001-06-14
PRIORITY APPLICATION NUMBER: 09/669,271
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/186,958
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Word 97
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
US-09-881-276-6

Query Match Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 FPSEBLWTS 12
DB 1 FFCALWPS 8

RESULT 11
US-10-417-895A-56
Sequence 56; Application US/10417895A
Publication No. US20040033369A1
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
APPLICANT: Capuccilli, Giido
TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
FILE REFERENCE: 1551-2002-001
CURRENT APPLICATION NUMBER: US/10/417,895A
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 60/373,686
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant peptide for third complementarity
OTHER INFORMATION: determining region of Fv region of an
OTHER INFORMATION: immunoglobulin
US-10-417-895A-56

Query Match Score 28; DB 15; Length 11;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 SFSEBLWTS 12
DB 1 SYSSWSS 9

RESULT 12

US-09-214-371-83
 ; Sequence 83, Application US/09214371B
 ; Patent No. US2001008511A1
 GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picklesley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal
 TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214-371B
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 83
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83
Query Match 40.3%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 6 FSDLW 10
Db 2 FSDLW 6
RESULT 13
US-09-732-384-4
Sequence 4, Application US/09732384
Patent No. US20020132971A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhi-Min
APPLICANT: Gu, Jijie
TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044
CURRENT APPLICATION NUMBER: US/09/732,384
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/169,816
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 10
SEQ ID NO: 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Protein
OTHER INFORMATION: Fragment not in inhibitory p53 polypeptide
US-09-732-384-4
Query Match 40.3%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 6 FSDLW 10
Db 2 FSDLW 6
RESULT 14
US-10-155-059-1
Sequence 14, Application US/10155059
Publication No. US2002014717A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/146,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-155-059-1
Query Match 40.3%; Score 27; DB 13; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 6 FSDLW 10
Db 2 FSDLW 6
RESULT 15
US-10-609-217-130
Sequence 15, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
APPLICANT: Feige, Ulrich
APPLICANT: Liu, Chuan-fa
APPLICANT: Cheetham, Janet C.
APPLICANT: Boone, Thomas Charles
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/609,217
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
; US-10-609-217-130

Query Match 40.3%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0;
 0; Gaps 0;
Qy 6 FSELW 10
 |:|
Db 2 PSDLW 6

Search completed: April 27, 2005, 16:01:24
Job time : 139 secs